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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 21:13:58 ; Search time 167 seconds
(without alignments)
9549.217 Million cell updates/sec

Title: US-08-978-277A-3

Perfect score: 5200

Sequence: 1 ATGGCGCAGCGAGTTCCAC.....CAGGCGCGTCCAGATGATTTC 5200

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq:*
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4: /cgn2_6/ptodata/2/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/Dackfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3903.4	75.1	5134	2	US-08-635-121-1
2	1920	36.9	6605	1	US-08-769-309A-4
3	1920	36.9	6605	3	US-08-994-570-4
4	99.8	1.9	7218	1	US-08-232-463-14
5	71.2	1.4	1926	4	US-09-249-585A-4
6	71.2	1.4	1931	2	US-09-130-114-2
7	70.8	1.4	1926	4	US-09-249-585A-2
8	70.8	1.4	2280	3	US-09-050-863-2
9	70.8	1.4	2580	4	US-09-359-081-2
10	70.8	1.4	5452	2	US-09-130-114-1
11	70.8	1.4	9600	4	US-08-910-647-1
12	70.8	1.4	9600	4	US-09-620-925-1
13	70.8	1.4	10596	1	US-07-884-811-15
14	70.8	1.4	10596	1	US-07-885-971-15
15	70.8	1.4	10596	1	US-08-087-783A-15
16	70.8	1.4	10596	1	US-08-194-088B-15
17	70.8	1.4	10596	2	US-08-194-087-15
18	70.8	1.4	10596	5	PCT-US93-04648-15
19	66.4	1.3	3489	2	US-08-728-323A-1
20	66.4	1.3	3489	4	US-09-298-568-1
21	66.4	1.3	32207	2	US-08-770-379-20
22	66.4	1.3	32207	4	US-08-757-669A-20
23	66.4	1.3	32207	3	US-09-230-371A-20
24	64.6	1.2	16442	3	US-08-781-891-208
25	60.4	1.2	2277	1	US-08-676-967-2
26	60.4	1.2	2277	1	US-08-676-974-2
27	60.4	1.2	2277	2	US-09-098-487-2

28	60.2	1.2	3337	1	US-08-072-610-1	Sequence 1, Appl
29	60.2	1.2	3337	2	US-08-719-822B-1	Sequence 1, Appl
30	60.2	1.2	3337	4	US-09-092-458-1	Sequence 1, Appl
31	58.8	1.1	51259	1	US-08-781-891-209	Sequence 209, App
32	56.4	1.1	3211	2	US-08-574-959A-8	Sequence 8, Appl
33	56.4	1.1	3211	4	US-09-357-014-8	Sequence 6, Appl
34	56.4	1.1	3901	4	US-08-574-959A-6	Sequence 6, Appl
35	56.4	1.1	3901	4	US-09-357-014-6	Sequence 1, Appl
36	55	1.1	1052	1	US-08-466-603-1	Sequence 1, Appl
37	55	1.1	1052	1	US-08-314-503A-1	Sequence 1, Appl
38	55	1.1	1052	1	US-08-468-066-1	Sequence 1, Appl
39	55	1.1	1052	2	US-08-466-717-1	Sequence 1, Appl
40	55	1.1	1052	2	US-08-466-743-1	Sequence 1, Appl
41	55	1.1	1052	5	PCT-US95-12414-1	Sequence 1, Appl
42	52.6	1.0	1505	3	US-07-915-246-1	Sequence 1, Appl
43	51.8	1.0	43795	3	US-08-742-185-101	Sequence 101, App
44	47.8	0.9	2518	4	US-09-433-699-3	Sequence 3, Appl
45	47.6	0.9	1276	4	US-09-177-325-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-635-121-1
; Sequence 1, Application US/08635121
; Patent No. 5910442
GENERAL INFORMATION:
APPLICANT: Gelman, Irwin H.
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,121
FILING DATE: 19-APRIL-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: A30558 - 165/33603
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5134 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-635-121-1
Query Match 75.1%; Score 3903.4; DB 2; Length 5134;
Best Local Similarity 97.5%; Pred. No. 0;

Matches 4120; Conservative 0; Mismatches 76; Indels 31; Gaps 14;

OY	984	GGAAAAAGCAGAGCCACCTCTCGAGAGGACGAGAGCCGGCAGAAAGCACAGACACAGCCAG	1043
Db	1	GGAAAAAGCAGAGCCACCTCTCGAGAGGACGAGAGCCGGCAGAAAGCACAGACACAGCCAG	60
OY	1044	GTGTGCACACATCTACAGAAAGGTGGAGCTGCTTTTGAAAGACAGGTGTGTGACTCTGA	1163
Db	61	GTGTGCACACATCTACAGAAAGGTGGAGCTGCTTTTGAAAGACAGGTGTGTGACTCTGA	120
OY	1104	GGCATCTGTCAAGAGAAAGTGTCTCTTTGGCAACGGAAGTGTGTGATGAGACATGGA	1163
Db	121	GGCATCTGTCAAGAGAAAGTGTCTCTTTGGCAACGGAAGTGTGTGATGAGACATGGA	180
OY	1164	AGCCCAACCAAAAGTGTGTGAGAGGTCCACGTGACACCGTGGAGAAACAGAGAGAGA	1223
Db	181	AGCCCAACCAAAAGTGTGTGAGAGGTCCACGTGACACCGTGGAGAAACAGAGAGAGA	240
OY	1224	GCAGGAGAGAGAGAGAGGCGTGAAGGGGCGTGTGTGTAAGAAACAAGAAATTCCT	1283
Db	241	GCAGGAGAGAGAGAGAGGCGTGAAGGGGCGTGTGTGTAAGAAACAAGAAATTCCT	300
OY	1284	GCCCCCTAGAAACTGTGCTGAGCCCCCAGAGAGGTCCCCCAGAAAGCGAGACCGTCAAGGA	1343
Db	301	GCCCCCTAGAAACTGTGCTGAGCCCCCAGAGAGGTCCCCCAGAAAGCTGAACCTGTCAAGGA	360
OY	1344	GCTGATGAAAGCAGAGAGATGTGTGTCTCTGGAGAGACCAACACTCACTACAGACCT	1403
Db	361	GCTGATGAAAGCAGAGAGATGTGTGTCTCTGGAGAGACCAACACTCACTACAGACCT	420
OY	1404	AAGTCCCTGAAGAGAAAGCGTCCGCCAAACCCAGAAAGCATATTGTACGTAGAGTGGACAT	1463
Db	421	AAGTCCCTGAAGAGAAAGCGTCCGCCAAACCCAGAAAGCATATTGTACGTAGAGTGGACAT	480
OY	1464	GCTGTCTCTCAGGAAAGAAATCAAGGTATCACAGGGAATCCTCTTGAAGAAACTTTCATAG	1523
Db	481	GCTGTCTCTCAGGAAAGAAATCAAGGTATCACAGGGAATCCTCTTGAAGAAACTTTCATAG	540
OY	1524	CTCAGGCTTTAAAGAACTGTCTGGGAAGAACGAAAGGGAAAACGAGAGGTGGGGAGA	1583
Db	541	CTCAGGCTTTAAAGAACTGTCTGGGAAGAACGAAAGGGAAAACGAGAGGTGGGGAGA	600
OY	1584	CGAAGAGCTTGGAAATACCAACATTCACACCGAATCCCCAGAGAGTGTGATGAGACA	1643
Db	601	CGAAGAGCTTGGAAATACCAACATTCACACCGAATCCCCAGAGAGTGTGATGAGACA	660
OY	1644	GAAAGGAGAGAGCTCTGCTGCTGCCGCCGAGAGAGCTGTGAGAGACCACTGTCTGGAGAA	1703
Db	661	GAAAGGAGAGAGCTCTGCTGCTGCCGCCGAGAGAGCTGTGAGAGACCACTGTCTGGAGAA	720
OY	1704	AGGGCCGCTGGAACACCCAGAGATGGGGAGGTGAGAAAGCACTCTCCGATGGAGA	1763
Db	721	AGGGCCGCTGGAACCA--CCAGGATGGGGAGGTGAGAAAGCACTCTCT--GTGA	775
OY	1764	GAAAGAGAGAGAGGATTCACCTCCCTGGGAGATCCTTCAAAAAGATGTGCACACCCAAANA	1823
Db	776	GAAAGAGAGAGAGGATTCACCTCCCTGGGAGATCCTTCAAAAAGATGTGCACACCCAAANA	835
OY	1824	ACGGGTCCGAAGACCTTCTGAGAGTACAAAGAGAGAAAGCTTGGAGAAAGTCAAGAGCGC	1883
Db	836	AC--GGTCCGAAGACCTTCTGAGAGTACAAAGAGAGAAAGCTTGGAGAAAGTCAAGAGCGC	894
OY	1884	CACCTTGTCTCCACTATATGACACAGTGTGAGAAATGCAAGATGAAAGTCAAAAAGCTTTGG	1943
Db	895	CACCTTGTCTCCACTATATGACACAGTGTGAGAAATGCAAGATGAAAGTCAAAAAGCTTTGG	954
OY	1944	TGAGAAACAAAAGCCAGAGAACCAAGCGTAGAGTGAATCTTCAAGTCTCTTGGGAAGC	2003
Db	955	TGAGAAACAAAAGCCAGAGAACCAAGCGTAGAGTGAATCTTCAAGTCTCTTGGGAAGC	1014
OY	2004	ACTGATTTGTGTCCGATATCTCAAGAAAGAGCAGAGAAAGCATCCTCTTCAGATGATGA	2053
Db	1015	ACTGATTTGTGTCCGATATCTCAAGAAAGAGCAGAGAAAGCATCCTCTTC--GAT	1071

OY	2064	AGGAGGCCAAGGACACTGGGGA -GGGAGACGTACAGACACAAAGAGGCCAGCAAAAGCA	21222
Db	1072	AAGAGGGCCAAAGGCACTGGGAGGGGGACAGTCACAGACCAAGAGAGGCCAGCAAAAGCA	11311
OY	2123	AAGAAGCCGGAACAGACGCTGTTCCTGTCAGACACCAGAGAGAGAACCAAGGCCAAGGAA	21822
Db	1132	AAGAAGCC -GAAACAGACGCTGTTCCTGTCAGACACCAGAGAGAGAACCAAGGCCAAGGAA	11800
OY	2183	GTTCCCTACCCGAGCCAGCGGGGAAGCCCTTCCGAAAGGGAAGGTGTCTCCACTTGGGAGT	22422
Db	1191	GTTCCCTACCCGAGCCAGCGGGGAAGCCCTTCCGAAAGGGAAGGTGTCTCCACTTGGGAGT	12500
OY	2243	CATTAAAAAGTTAGTACACTCCAAAGAAAAAATCCAAAGTCAAAACTGGAAAGAAAGCCG	23022
Db	1251	CATTAAAAAGTTAGTACACTCCAAAGAAAAAATCCAAAGTCAAAACTGGAAAGAAAGAG	13100
OY	2303	AAGACTAGTGTAGAG ------CAGTGTGTCCACTGAGTGCAGAACCGAGTAGAGAA	23542
Db	1311	CCGGAGAGACTCTAGTGTAGAGAGCAGGTGTGTCCACTGAGTGCAGAACCGTGTAGAGAA	13700
OY	2355	ATCTTGCGTTTCCATTAAAGAAATTCATCCCCGAGCGCGGGAAGAAAGGCAAGACGGAA	24142
Db	1371	ATCTTGCGTTTCCATTAAAGAAATTCATCCCCGAGCGCGGGAAGAAAGGCAAGATGGAA	14300
OY	2415	-GCAAGAACCAAGCCACTGTGTGAAGACTCAGGGCCAGTGGAGTAAATGAGACGACCTTA	24733
Db	1431	GGCAAGAACCAAGCCACTGTGTGAAGACTCAGGGCCAGTGGAGTAAATGAGACGACGCTG	14900
OY	2474	ATGTGTCCAGCCGTGTGTCTCTGTCTGTAGATATATGTAAGTGAAGAGGGAAGATGGAG	25333
Db	1491	ATGTGTCCAGCCGTGTGTCTCTGTCTGTAGATATGTAAGTGAAGAGGGAAGATGGAGAG	15500
OY	2534	CCCAAGGGGAATACGAGACTCTCCCACTCTCTGGGGCGCTGTACCTGTCCAGAGAGCTCA	25933
Db	1551	CCCAAGGGGAATACGAGACTCTCCCACTCTCTGGGGCGCTGTACCTGTCCAGAGAGCTCA	16072
OY	2594	GTAAGACTCTGTGTCCACACTGTGATGTGTGCAGTCAATTGATGGAGACAGGCACTACCA	26533
Db	1608	GTAAGACTCTGTGTCCACACTGTGATGTGTGCAGTCAATTGATGGAGACAGGCACTACCA	16672
OY	2654	GTCGTCAAGAGACGGTGTCTCTTGGGATPPTCCGCTTCCGTAACACACCTCTTGAACCA	27133
Db	1668	GTCGTCAAGAGACGGTGTCTCTTGGGATPPTCCGCTTCCGTAACACACCTCTTGAACCA	17272
OY	2714	CAGCGGGAAGAGCCATCCACACTGTTGAAGAGTCACTGAAAAAGACATCTTGCAGAG	27733
Db	1728	CAGCGGGAAGAGCCATCCACACTGTTGAAGAGTCACTGAAAAAGACATCTTGCAGAG	17872
OY	2774	AAACTCTGTGTCTACCCACACCTTACAGAGGGTAAAGATCCCATAGACACATGGTCA	28333
Db	1788	AAACTCTGTGTCTACCCACACCTTACAGAGGGTAAAGATCCCATAGACACATGGTCA	18472
OY	2834	CCAGTGAAGTGAATTTACCTCAGAGCTGTGTACAGCCACAGAGACCTCAGAGGCTCTCC	28933
Db	1848	CCAGTGAAGTGAATTTACCTCAGAGCTGTGTACAGCCACAGAGACCTCAGAGGCTCTCC	19072
OY	2894	GTACTGAAGAAGTTACCGAAGCATTCGGGGGCGGAGAGACACACAGACATGTGTCCGAG	29533
Db	1908	GTACTGAAGAAGTTACCGAAGCATTCGGGGGCGGAGAGACACACAGATGTGTCTCCGAG	19672
OY	2954	TTTCCCAAGCTGACGTACTCTCCCAAGACACACAGAGAACCCACCCAGTTCAGGAGGTAG	30133
Db	1968	TTTCCCAAGCTGACGTACTCTCCCAAGACACACAGAGAACCCACCCAGTTCAGGAGGTAG	20272
OY	3014	AGAGTGTGTGTAGATACAGAAAGAGAGAGGCGCAGACGAGGCGCATCTCTCAAGCGG	30733
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3314 CAGATGTAGACATGTGCGCCAGCTGCGAGTTATCAAGCTCCAGAGCTGATGAAACAGG 3373
2328 CAGATGTAGACATGTGCGCCAGCTGCGAGTTATCAAGCTCCAGAGCTGATGAAACAGG 2387
3374 CCGTGGCCCTGAGTCTATCCGAAACCTTGACACACAGTGAACAAATGGAAGCACTCCCT 3433
2388 CCGTGGCCCTGAGTCTATCCGAAACCTTGACACACAGTGAACAAATGGAAGCACTCCCT 2447
3434 TACAGATTCAGACATGCGATGGGACACAGAGATGAACCATTTGACAGCAGAGACA 3493
2448 TACAGATTCAGACATGCGATGGGACACAGAGATGAACCATTTGACAGCAGAGACA 2507
3494 GTAAAGCCACTGAGCTGTCTAGGCACTCAAGGTCAACAGAGAGAGAGCGCTACTGCTC 3553
2508 GTAAAGCCACTGAGCTGTCTAGGCACTCAAGGTCAACAGAGAGAGAGCGCTACTGCTC 2567
3554 AGAAAGAGAGCTTTGACACTCTATATATTTTCCAGCCCAAGAGAAACATGGGGAG 3613
2568 AGAAAGAGAGCTTTGACACTCTATATATTTTCCAGCCCAAGAGAAACATGGGGAG 2627
3614 AACGAGAGAGATGTTCTTGAACACTACACAGAGAGCTTACTGCTGACGCGCTGCGC 3673
2628 AACGAGAGAGATGTTCTTGAACACTACACAGAGAGCTTACTGCTGACGCGCTGCGC 2687
3674 TTTCTGCAAGAGCTGAGTGGTGTCAAGAGGGTGAAGTTGATGATGAGAGAGAG 3733
2688 TTTCTGCAAGAGCTGAGTGGTGTCAAGAGGGTGAAGTTGATGATGAGAGAGAG 2747
3734 TCAAAAGAGAGAGAGTGTGTTGACACTCTGAGACCCCAAGTCAAAAGGCTGCTGATG 3793
2748 TCAAAAGAGAGAGAGTGTGTTGACACTCTGAGACCCCAAGTCAAAAGGCTGCTGATG 2807
3794 TGAATATGACATGAGTGAAGTGTGAGAGAGGAGAGTGAACCTGATGAAAGAGAGAGTGAAG 3853
2808 TGAATATGACATGAGTGAAGTGTGAGAGAGGAGAGTGAACCTGATGAAAGAGAGTGAAG 2867
3854 TGCAGAGCTTTAGCTGAGAGAGGAGAGAGTGAACCTGATGAAAGAGAGAGTGAAG 3913
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3914 AGCAAAAGCAGAGAGAGTGTGTTGACACTCTGAGACCCCAAGTCAAAAGGCTGCTGATG 3973
2928 AGCAAAAGCAGAGAGAGTGTGTTGACACTCTGAGACCCCAAGTCAAAAGGCTGCTGATG 2987
3974 AAGCAACTACAGGAGAGAGAGTGTGTTGACACTCTGAGACCCCAAGTCAAAAGGCTGCTGATG 4033
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4034 CACTGGGAGAGCTTTGAGAGAGAGCTTCTCCAGAGAGAGAGAGAGAGTGTGATG 4093
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4094 AGTTTCAAGTTCAGAGAGCTGAGAGAGAGTCACTCAAAAGAGAGAGAGTGTGATG 4153
3108 AGTTTCAAGTTCAGAGAGCTGAGAGAGAGTCACTCAAAAGAGAGAGAGTGTGATG 3167
4154 TCATAGAAAGCGTTGATTTTCAGAGAGAGTGAAGTCCAGAGAGTGTGATG 4213
3168 TCATAGAAAGCGTTGATTTTCAGAGAGAGTGAAGTCCAGAGAGTGTGATG 3227
4214 TATTACAGCTGAGAGAGTCTCTGCAAGCGGTGGCCACTGAGACTTTGACAGCATGAGAG 4273

3228 TATTACAGCTGAGAGAGTCTCTGCAAGCGGTGGCCACTGAGACTTTGACAGCATGAGAG 3287
4274 ACAGGCTACCCCTGGGGGCTGAGTCTCAGGAGAGATCCATCCATCATATGTAACCTG 4333
3288 ACAGGCTACCCCTGGGGGCTGAGTCTCAGGAGAGATCCATCCATCATATGTAACCTG 3347
4334 CTCCTGAAGACACCTTACATCTGAGCTTCAAGAGAGATTAAGCGATCCAGAGAGAG 4393
3348 CTCCTGAAGACACCTTACATCTGAGCTTCAAGAGAGATTAAGCGATCCAGAGAGAG 3407
4394 GATCAG 4453
3408 GATCAG 3467
4454 CAATCGAAAAAGTCTTCAAGAGTGAACCTGAGTCTGCACTGAGAGTGAAGAGACACA 4513
3468 CAATCGAAAAAGTCTTCAAGAGTGAACCTGAGTCTGCACTGAGAGTGAAGAGACACA 3527
4514 AGATGTGGTGAAGAGTCAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4573
3528 AGATGTGGTGAAGAGTCAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3587
4574 CCGAACTCATGCTTATGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4633
3588 CCGAACTCATGCTTATGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3647
4634 AGCCCAAGAGAGTCTGAG 4693
3648 AGCCCAAGAGAGTCTGAG 3707
4694 CAGAGAGAGAGTCTGAG 4753
3708 CAGAGAGAGAGTCTGAG 3765
4754 TGCAGGCTTGCAGTGAAG 4813
3766 TGCAGGCTTGCAGTGAAG 3825
4814 ACCCAAGAGTCCAAAG 4873
3826 ACCCAAGAGTCCAAAG 3884
4874 CAGAGAGAGAGTCTGAG 4933
3885 CAGAGAGTCTGAG 3941
4934 TAAACGAG 4993
3942 TAAACGAG 4000
4994 CAGTCAAG 5053
4001 CAGTCAAG 4060
5054 CAGATCTTAAG 5113
4061 CAGATCTTAAG 4120
5114 TCACAG 5173
4121 TCACAG 4179
5174 CAG 5200
4180 CAG 4206

RESULT 2
US-08-769-309A-4
; Sequence 4, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:

Db 432 CTAAATGCCAGAAAGAGCCCTGAACGGTCAAGAGCCCTAAACACCCAGAGAGAA 491
QY 247 GAAGTGTGATGATGATGATGTGGACAGCCAGATCAGAGATGTGAGAAAAAGCCGA 306
Db 492 GAAGTATTGTACAGGAGGTGGACAGAGACTGTGAAGATGTGAGCAAGAAAGACTCC 551
QY 307 GTTGAAGAAATGGCGGCCAACTCCACAGCTGTTGAAGATTCACAAAGATGGGACGAG 366
Db 552 GATAAAGAGATGGCTACTAAGTCAGGGGTTGTTACAGACATCCACATGATGGGACGAG 611
QY 367 GAGACATCAGAAATTAATGAACAGATCCCTGCTTGAAGAAAAACAATGTGGAAGAAATGTA 426
Db 612 GAGA---ACCGAATATCAACAGATTCCTCTTCAGAAAGCAATTAGAAGAGTAAACA 668
QY 427 CAGCCTGTGAGTCCCAAGCTATGATGTTGGCTTCAAGAAATATTTAATTTGTTGGT 486
Db 669 CAACCCACTGAGTCCAGGCTAATGATATTGATTTAAGAAAGGTGTTTAAAGTTGTTGGC 728
QY 487 TTTTAAATTCACGTGAGAAGATTAATAAATGAATAAGTCAAGATCTGCCAATCTACT 546
Db 729 TTTTAAATTCACGTGAAAAAGATTAAGACAGAAAGCCTGACACTGCCAGTACTCAGT 788
QY 547 GTCAAGAGAGATGAAGCGCAAGGGGCGAAGAGCCTGCTGTGGAGCTGAGACACCAAGAG 606
Db 789 GTGAAGAAAGATGAAGGGAGGAGCAGCA-----GGGGCTGGCAGCACCAAGAGAC 839
QY 607 CCCAGTGTGAGAGCTGCCCTGGAGAGTCAAGCTTCCAAAGAAAGTGAAGCTGAAGCAATCC 666
Db 840 CCCAGCTTTGGGGCT-----GGAGAGCAGCCTTCAAAGAAAGCAACCCAAACATCT 893
QY 667 ACAGAGAAACCAAGAGAGCACCCTGAAGCAAGACAGAGCAGCACAAATATCCCTTTCAA 726
Db 894 ACAGAGAAACCGAAGAGAGCCTGAAGCGTGAAGCAAAAGCCAGCACAATTTCTCCCCA 953
QY 727 GCCGAATCTGATCAGCGCTGAGAAAGAACCAAGATGAAGAGAGAAAAACAAGAG 786
Db 954 GCCGAATCTGGCCA---GCAGTGGAGAAATGCAAAAGAGAAAGAGAAAGAAACAAGAA 1010
QY 787 AAAGAGCCCAACCAAGTCCCGAGATCCCGAGAGCCCAAGTCAACATGAGAACATCT 846
Db 1011 AAAGAACTTAGCAAGTCTGAGATCTCCGACTAGTCCGTGACCAAGTGAACAGATCA 1070
QY 847 TCCCTTCAAGAGTTCTTCACTACGGTTGGGCGGCTGGCGCAAGAGACACACTTCAAG 906
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QY 967 GTAGACGAGAGAAAGAAAGAAAGACAGAGCCAGCTCGGAGAA----- 1010
Db 1191 GTAGACAGAAAGAAAGAGAAAGAGAGGTTGCTCCGAGAACTGACCGCTCCGAG 1250
QY 1011 -----GCAGAGCCCGGCGAGAGACACAGACAGGCCAGCTTGTTCAGAGACTAC 1059
Db 1251 CAAGCCCAACCAAGSAGGCGGAGAAAGTGCACACAGAGACCCCGTTATTCAGTGAATAT 1310
QY 1060 GAGAGAGTGAAGCTGCTTTTGAAGACCAAGTTGTGACCTGAGAGCATGTCAGAGAG 1119
Db 1311 GAGAAAGTTGAGTCCCTCAGAGAGAGCAAGTCAAGTGTGCTCGAGACCTTCTGAAGAG 1370
QY 1120 AAGTGTGCTCTTTGGCAAGGAGTGTGATGAGAAATGGAATGGAACCCACCAAGAA--- 1176
Db 1371 AAACCTGCTCCGTGGCAGACAAAGTGTGATGAGAAATTAAGAAATTCACCAAGAAAGAG 1430
QY 1177 GTTGTGACAGAGTCCACGTGACACCGTGAAGAGACAGAGAGAGAGAGAGAGAGAG 1236
Db 1431 GTTGTGGCGAGATCCAGCTCAGACACCGTGAAGAGAGAAACGAAGAGAGAGAAAC---- 1486
QY 1237 GAGAGAGCTGAAGGGGGCTGTGTGAGAGAAAGACAGAAATCTTTGCCCTTGAGAAA 1296
Db 1487 -----GGAGGTGGAAGAAACAGCAGGGTCTGTGCCAGCTGAAGAA 1526

QY 1297 CTGGCTGAGCCCGAGAGGTCGCCAGAAAGCTGACCTTGTGAGAGAGCTGATGAAGAC 1356
Db 1527 TTGGTGAATGATGATCAGAACTCAGAGAGCCGAACCTCCAAAGAGCTGGGAGACTC 1586
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QY 1417 AAGACCTGCCCAACACCCAGAGAGCATTTGTCAAGTGAAGTGAAGTCTGTCTCAG 1476
Db 1647 AAGTGTCTGTCCAAACCCCGAAGCGTGTGAGTGAAGTGAAGTGTGTCATCAGAG 1706
QY 1477 GAAGAAATCAAGTACAGGAAGTCCCTGGAAGAAACTCTTCAGTAGCTCAGGCTTAAAG 1536
Db 1707 GAGAGATGAAGGTGAGAGGAGTCACTAAAGAACTTTTATTCAGACACTGGCTTAAAA 1766
QY 1537 AAGCTGTGGAGAAAGAGAGAGGGGAAACGAGAGGTGGGAGAGACGAAGAGCTTGA 1596
Db 1767 AAGCTTTCTGGAAGAAAGAGAGGGGAAAGAGAG---GGAGAGACAGAGAAATCAGGG 1823
QY 1597 GAATACCAACACTTCAACCCGAATCCCAAGAGATGCTGATGAGCAGAGAGAGAGAGC 1656
Db 1824 GAGCAACTCAGGTTCCAGCCGATCTCCGAGACAGCAGAGAGAGCAAAAAGGCGAGAGC 1883
QY 1657 TCTGCGTCCGCCCCGAGAGCCTGAGAGAGACACGCTGTCTGGAAGAAAGGCCGCTGAA 1716
Db 1884 TCTGCTCATCTCCCTGAGAGGCCGAGAGANTCAGTGTCTGGAAGAAAGCCTTAGCCGAG 1943
QY 1717 GCACCCAGAGATGGGAGAGCTGAGAGAGAACTACTTCCGATGAGAGAGAAAGAGAGAA 1776
Db 1944 GTCCACAGAGATGGGAGAGCTGAAGAAAGAGAGTACTTCCGATGAGAGAGAAAAAGAGAA 2003
QY 1777 GGGATCACTCCCTGGCATCTTCAAAAAGATGTGACACCCAAAGAACGGGTCCAGAA 1836
Db 2004 GGTGTCACTCCCTGGGCATCATTCAAAAGATGTGACGCCCAAGAAAGGTGTTAAGCCG 2063
QY 1837 CCTTCTGAGGTGACAAAGGAGGAGAGCTGGAAGGTCAAGAGGCCCACTGTGCTCC 1896
Db 2064 CCTTGGAAAGATATGAAGATGAAGTGTGACAAAGGTCAAGAGCCCTACCTTGTCTCC 2123
QY 1897 ACTGATGACACAGTGTCAAGAAATGCAAGATGAAGTCAAAACTTTGTGAGAAACAAAG 1956
Db 2124 ACCGAGAACACACCTCTGAATGCAAGAAAGAAATGAAGGAGCGGTGAAGAGCCAAAG 2183
QY 1957 CCAGAGAACCAAGCGTAGGTGATPACTTCAGTCTTTGGAGACACTGATTTGTCTC 2016
Db 2184 CCGAGAGAACCAAAAGCGCAAGGTGATPACTTCAGTCTTTGGAGACCTTAAATTTGTGTG 2243
QY 2017 GGTATCATCCAAAGAGAGCAGCAAGAGGCACTCTTTCAGATGATGAAGAGGCGCAAG 2076
Db 2244 GGTATCATCCAAAGAAAGAGCAGAGAGGTCCTTCTGTATGAGAGGGGACCAAAA 2303
QY 2077 ACACCTGGAGGGGACAGTACAGAGAGAGAGAGGAGCCAGCAAAAGACAAAGCCGAGACA 2136
Db 2304 GCATGTGGAGAGAGACACCAAGAAAGCTGAATGAGGCCGGAAGAACAAAGAGAGAGGAGACA 2363
QY 2137 GACGCTGTCTGTCACAGACCAAGAGCAGAGCAAGCCAAAGCCAAAGATTTCTACCCGAG 2196
Db 2364 GACGGATCTGTTGCTGTTTCCCAAGAACATGATCCAGGCGAGGAGAGATTCCTCCCGAG 2423
QY 2197 CCAAGGGGAAAGCCCTTCCAAAGGGAAGGTCTCCACTTGGAGATCTTTAAAGATTA 2256
Db 2424 CAAGCTGGAAGCCCTTACCAAGAGGAGGCGGCTTCCACTTGGAGATCTTTAAAGATTA 2483
QY 2257 GTCACTCCAAAGAAAAAATCCAAAGTGAAGAGAGAAAGCCGAGAAC----- 2307
Db 2484 GTACGCCCAAGAAAAAATCAAGTCAAGCTGGAAGAGAAAAAGCAAGACATCCATAGCT 2543
QY 2308 ---TCTAGTGAAGCAGTGTGCTCACTGAGATCAGAACGAGTAGAGAGAAATCTTGGGTT 2364
Db 2544 GGCTGTGTTGATGACATTCACACTCAGACACTCAGACCCGGTTAAGAAAGATCTGTGGTTC 2603

OY	2365	TCGTTTAAAGAAATTCAATCCCCGAGCGGGAAAGAAAGGCGACGACGGGAAACCAAGCA	2421
Db	2604	TCGAATCAAGAGATTATTTCTGTGACGACGAGAGAAAGAAAGGCCAGATGGGAAACAAGAACAA	2663
OY	2425	GCCACTGTGAAAGCACTCAGAGGCGCAGTGGAGATTAATAATGAGAGCAGACCTTAATGTCCACGC	2484
Db	2664	GCCTCTGTGAAGACGAGGGGCCAACAGGGGCCAACGAAAGATGACTCTGATGTCTCCGGCC	2723
OY	2485	GTCGTGCTCTGTCTGAGTAAATGCAATGGAGAGGAGGAGAGATGG-----AGGCC	2535
Db	2724	GTGTGCTCCTCTGTCTGAGTATGATGCTGTGAAGAAAGGAGAAATATGAGAGCACACAGAGCC	2783
OY	2536	CAGGGGAATACGAGAGCTGCCCCAGCTGCTGGGGGCTGTCTACGTCTCCGAGAGACTACGT	2595
Db	2784	CAAAAAGCGCAGAGCGAGCCCGAGAGAAAGGACAGCCACTGAGGTCTCCAAAGAGCTCAGC	2843
OY	2596	AAGACTCTGGTCCACACTGTGAGTGTGCGCAGTCAATTGATGGAGCAGGCGAGTCACAGT	2655
Db	2844	GAGAGTCAGGTTCATATGATGGCAGCAGAGCTGTCTGACGGGACAGGGGCAAGTACCATTT	2903
OY	2656	GTCGAGAGCGGTCTCCCTTGTGGATATCCGCTTCCGTAACGAAGCTTTTGAACACACA	2715
Db	2904	ATTGAAGAAGAGTCTCCTCTTGGATATCTGCTTCACTGACAGAACCTTTGAACAAAGTA	2963
OY	2716	CGGGAGAGAGCCATGCGCACCCTGTTTGAAGAGTCACTGGAAGAAAGACATATTTGC---AGAA	2772
Db	2964	GAACTGTAAGCCGACGCTGTTAACTGAGGAGGATATTTGAAGAAAGAAATATTTGCGAAGAA	3023
OY	2773	GAAACTCCTGTGTCTCACCCGACAGGTTTACAGAGAGGTAAAGATGGCCCATGACAGACATGGT	2832
Db	3024	GAACTCCCAACAGTGTACTGAACTCTGTCCAGAACACAGAGAGAGCCCGGGGGCGACAGGTCTC	3083
OY	2833	ACCASTGAAGTGAATTTTCACCTCAGAGAGCTGTACAGCCACAGAGACCTCAGAGGCTCTC	2892
Db	3084	GTTAGTGAAGCGGGAATTGACCCCCGAAAGCTGTGACAGTCTCGAAGAACTGCAAGGCCATTGG	3143
OY	2893	CGTACTGAAGAAATTTACCGGAAGCATGTGGGGGCCGGAAGAGACACAGACATGGTGTCCGCA	2952
Db	3144	GGTTCGGAAGAAAGAACCCGAAGCATCTGTCTGTGAAGAAACACAGAAATGGTGTCAAGCA	3203
OY	2953	GTTTCCCACTGAGTGTGATCTCCACAGACACACAGAGAAAGCCACCCAGTTTCAGAGAGTA	3012
Db	3204	GTCTCCCAAGTTTAACCCAGCTCCCAAGACACACAGAGAGAGGCCATCTCCGGTCCAGAGAGTG	3263
OY	3013	GAGAGTGGTGTGCTAGTATACAGAGAAAGAGAGAGCGCCAGACGACGAGCCATCCTCCAAACC	3072
Db	3264	GAAGTGGCGTACCTGACTACATAGAAGAGCAAGAGAGAGCGGACTCAAGAGAGTCTCTCAGAGCA	3323
OY	3073	GTTGCAACACAAAGTGAAGAGAGAGTCCCAAGTGTCTCTGCACAC---CAGACTGTGCAGAGA	3129
Db	3324	GTGGCAGAAAAAGTGAAGAGAGGAATCCCAAGCTGTCCGGACCGGTGGGCCCAAGAAATGTG	3383
OY	3130	ACGGGGCTAAAAAGCATCTGGAGAAAGGTTGAGAGAGGTGAGAGAGACTCCGAAGTGTGGCT	3189
Db	3384	CTTCAGCCTGTGCAAGAGAGGACAGAGGCGCAAGAAAGCAGAAAGACAGAGCTGAAAGCTCGGGCT	3443
OY	3190	TCGGGAAAGAGAGAGAGAGCTTATGTCCGGAAGAGACCCGTCAGAGAGCTGAGAGTGGAGAT	3249
Db	3444	CTGAAGAAAGAGAGAGGATGTATAGTGTGTAAGATGTATGATGTCTCAAGAGAGCAAAAAATGTAGCT	3503
OY	3250	CTTGCAACAGGSGCTGTGAGACTGGAAGAGGCTACTTCCAGAGAGCCTTGG---AGTTCTGTGA	3306
Db	3504	TTTACACAAAGGAGAGTGTGTGGGGGAGACACCCTCCAGAAAGCTTTGAAGAAAGCTCTCAAA	3563
OY	3307	GTCACGCGCAGATGA-----GACCAATGTCTGCCACTGGCA-----	3341
Db	3564	GTCAACAGAGACATATAGAGTCCAGTGAAGCTTTGTAAACCACTGTGTCAAGCCGAAAACCTTTAGCT	3623
OY	3342	--GGTTATCAAGCTCCAGAGAGCTGATGAAGAACAGAGCCGTGGCCCCCTGAGTCAATCCCAAC	3399
Db	3624	GGGGTAAATATCACAGAGAGATGTGTATGGAAGACAGGCTATATCCCCCTGTACTCGGTGCAAAAC	3683
OY	3400	TTTGACAGCACTGAGACAAATGGAAGCACTCCCTTAGCAGATTCAGACACTGACAGATGG	3459

Db	3684	CCTACAGACAGTGTGACCTGATGTGAGACACCCCGTATGCGGACTTTGGACGACACAGACGACA	3743
Qy	3460	ACACAGCAAGATGAAACCATTTGACAGCCAGACAGTAAAGCCACTGCAGCTGTACAGCGAG	3519
Db	3744	ACCCAGAAAGACGAGATTGTGGAAATTCATGAGAGAAATGAG---GTGCATCTGTGTACCA	3800
Qy	3520	TCACAGCTCACAGAAAGAGGCGGCTACTGCTCCAGAAAGAGGACCTTCCACACTACTCT	3579
Db	3801	GTCAAGGGCCACAGAAAGCAGAGGAGATTTCTGTGCACAAAGAGAGGCTCTCCAGACCTTCC	3860
Qy	3580	AATAATGTCTCCAGCCCGAGAAACATATGGGGAAGAACCCAGGAAGAGATGTCTTTCACCT	3639
Db	3861	AGTTTGTGTTCCAGGAAGAACTAAAGAACTCAAAATATGGAAGACACTCTAGACAT	3920
Qy	3640	ACACAGCAAGACTTACTGCTGCAGCCGTGCCCCGTTCTGGCAAAAGCTGAGGTGGTCAA	3699
Db	3921	ACAGATTAAGAGGCTGTCAAGTGGAAAGCTGTATCCATCTGTCAAGAGCTGAGGGGACTCAA	3980
Qy	3700	GAGGCTGA-----GTTTGCAGTGTGGATGTGAGAAAGAAAGTCAAGAGAACAGAG	3750
Db	3981	GAGGCTGCACGATGTGCTGATGAGAAACCAGAAAGCGTACACTTTTGGAGAGCACTTGA	4040
Qy	3751	GGTTTGTACACTCTGG-----ACCCACAGTCAAAAGCGTGTGATGTGCATATATAC	3804
Db	4041	GGGTTATATGACACAGCAGCATTAACGTCTAGTGGGAAAGGCTACTGAACTGCTTAA	4100
Qy	3805	AGTGAAGTATGGGAGTGGCGGGGTGTCAAGAAAGAGAGTACTGAAGTGCAGAGTCTT	3864
Db	4101	GSTGAAGGACAGAAAGAAAGCGTAAATGTAAAGAGATGATGCTTTGAAGTCCAGAGTCA	4160
Qy	3865	-----ACCTTGGAGAGGAGAGATGGAAGTGCAGTGTGAAAGAGAA	3909
Db	4161	GCTAAGTCTCCTCCATCCCGCTGGTGGAGAGAGATGTGTTCATAGTCCAAAGGAGAA	4220
Qy	3910	AGGGAGCAAAAGCCAGAGCAAGTAGTGAAGAAAG---TGAGAGAGAAACAGCCGCTCT	3966
Db	4221	ACAGAGCAGAGCCACCCATGTGTAATGAAGAAAGACTTGAAGACGAAGACCTTACC	4280
Qy	3967	GAGCATGAGAGAACCTCAGGGGAAGCCAGTCTCTGACACTTGAATGCCAGCTCAGAGAG	4026
Db	4281	GTATCTGAAGAGGTCAGTAAGACAGCTCTCCACAGAGTGAATGTGCCATCATATAGATGG	4340
Qy	4027	GGGAAGCAGTGGGAAGCTTTGGAGAGAGCCCTTCTC---TCCAGACCAAGACAAAGCA	4083
Db	4341	GCAAGGGAAGTCAACAGCTTTTGAAGAGAGCCCTCTCTCCCTGTAGTCTCAAGAGAGCA	4400
Qy	4084	GSTTCCATAGAGGTTCAAGTTTCAAGCGTGGACACAAAGTCACTCAACACAGCAAGCT	4143
Db	4401	GTATCTACCAAATTCAGATGTGAGGCTCTGAAGCATCATCTCTTAACAGCGCTGCA	4460
Qy	4144	GTGGAAGAGTGCAT-----AGAAAGCGTTGTATTCTAGAGACAGGTGAAGTCCAGAG	4197
Db	4461	GAGGAGGAAAGAGCTCTTAGAGGAAGAACTGCCACAATTTTGAAGAAAGGTGAAGCGTGGAG	4520
Qy	4198	TGTGTAGGTGCACACTTATTACACAGCTGAGAGATCTCTGCAAGGGGTGGCCACTGAGCT	4257
Db	4521	CCTGCAAGGTGCACATTTAGTTTCTGGAAGAGAAATCTGTGAAAAAATTAAGACATTTGCC	4580
Qy	4258	CTTTCAGCATGCAAGAGACAGGATACCCCTGTGGGCGCTGAGTCTCAGGCAGAAATTCATCCA	4317
Db	4581	GCTCATCCAGGGGAAGATGCTGTGCCACAGGGGCCGAGCTGTCAAGCAAAATTCGACACA	4640
Qy	4318	ATCATAGTAAGTCTCTGCTCTGAAAGACCCCTACATCTGAGACTCAAGAGAAATTAAGC	4377
Db	4641	GTGATATGATTTGCTACTTACCAGAAAGGCTTTAGTTTCCGAGCTGGAAAGAGAGAAAAAC	4700
Qy	4378	GCATCCAGAGAGAGCATCAGAGGAAGAGAGACCAAGATGCTGGTCTGTATCTGATCAGAC	4437
Db	4701	ACATATCATGAAGTGAAGTGAATGAAGTGTGATGAGCAGAGGTTGCTTGCC-----AGAG	4754
Qy	4438	GGCAGAGAGCTACGCAATTCGAAAAAGTCTTAAGGCTGAAGCTGATCTGTGCACTT	4497

[illegible]

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RESULT 4
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 diagonal Road, Suite 500
City: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0., Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BEWT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZ9pt-F1s
US-08-232-463-14
Query Match 1.9%; Score 99.8; DB 1; Length 7218;
Best Local Similarity 2.1%; Pred. No. 4,7e-15;
Matches 8; Conservative 262; Mismatches 109; Indels 0; Gaps
QY 912 AAAAGAGATGATCTCGAAACTGCAGAGAGAAGAAAGAGCAAGACGAAGAAAAGTACA 971
DB 1431 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1372
YY 972 CGAGGAGAAAAAGAAAAAGACAGAGCCAGCCTTCGGAGAGAGCAGAGCCGCGAAGAACAC 1031

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[illegible]

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RESULT 5
US-09-249-585A-4/c
: Sequence 4, Application US/09249585A
: Patent No. 6417002
: GENERAL INFORMATION:
: APPLICANT: Horlick, Robert
: TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
: FILE REFERENCE: 0867/0D905
: CURRENT APPLICATION NUMBER: US/09/249,585A
: CURRENT FILING DATE: 1999-02-11
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Patentin version 3.0
: SEQ ID NO: 4
: LENGTH: 1926
: TYPE: DNA
: ORGANISM: Epstein Barr Virus
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (1)..(1926)
: OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

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	Query Match	Similarity	1.4%	Score 71.2:	DB 4:	Length 1926:
	Best Local Similarity	47.7%:	Pred. No.	3.8e-08:		
	Matches 208:	Conservative	0:	Mismatches 228:	Indels	Gaps
QY	948	GGAGCAGGAGCGCCAGAAAAAATGTACGAGGAGAAGAAAAGCAAGAACAGACCAGCTCCGA	1007			
Db	977	GGAGGACGAGGAGCGGGGAGACGACGAGGACGGGGAGGAGCACGAGACCGGGAGACGGGA	918			
QY	1008	GGAGCAGGAGCCCGGCAGAAACACACAGACCAGGCCAGTTTTCACGACAGACTCAGAAAGT	1067			
Db	917	GGAGCAGGAGCCGGGAGGAGCGGGGAGAGACGAGAGCCGGGAGGAGCAGCGGAGAGCAGAGACGG	858			
QY	1068	GGAGTGCCCTTTGGAAGACCCAGGTTGGTGACTCGAGCATGTGTACAGAGAAATGTGC	1127			
Db	857	GGAGGACGGGGAGGAGGACGAGGACGGGGAGGACGGGGAGGAGCAGGAGCGGGAGAGA	798			
QY	1128	TCTCTTGGCCAACGGAAGTGTATTGATGAGAAGATGGAACCCCACAAGAAGTTGTTGCAGA	1187			
Db	797	CGGGAGGACGACGAGACGGGGAGACGGGGAGACGACGAGGACGGGGAGGACGGGAGGACGA	738			
QY	1188	GCTCCACGTGAGCACCCGTGAGAAAGACAGAGGAGGACGAGGAGGAGGAGGAGAGAGCTGA	1247			
Db	737	GGAGCGGGAGGACGAGCAGCGGGGAGGAGGAGGACGGGGAGGAGCAGAGCGGGAGGAGACGG	678			
QY	1248	AGGGGCGCTGCTGGTAGAAGGAGACAGGAGAAATCTTGGCCCCCTGAGAAACTBTGAGACC	1307			
Db	677	GGAGGACGGGAGGAGGAGCAGAGACGAGGAGGAGGAGCAGGAGGAGGAGCGGGAGGACGG	618			

[illegible]

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RESULT 6
US-09-130-114-2/C
; Sequence 2, Application US/09130114
; Patent NO. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaji, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/ID90351
; CURRENT APPLICATION NUMBER: US/09/130, 114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

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Query Match	1.48;	Score 71.2;	DB 2;	Length 1931;
Best Local Similarity	47.78;	Pred. No. 3.8e-08;		
Matches 208; Conservative	0;	Mismatches 228;	Indels 0;	Gaps 0;

QY	948	GGACGACAGAGCCACAAAAAAGTATGACGAGGAAGAAAAAGAACACAGAGCCAGCCTCGGA	1007
Db	977	GGAGACGACGAGACCGGGAGGACGAGCGACGGGGAGGAGACGAGACGCGGGAGGACCGGGA	918
QY	1008	GGAGCAGGAGCCCGGCAGAAACACAGCACCGGCCAAGTTGTACAGCACTACGAGAAAGT	1067
Db	917	GGACGAGGACCGGGAGGAGCAGGGGAGAGACGAGACCGGGAGAGACGAGAGACCG	858
QY	1068	GGAGCTGCCCTTTGGAAACACCAAGTTGGTGTACCTGGAGGCATCCTCAGAGGAGAAGTGTCC	1127
Db	857	GGAGACACGGGAGGAGGACACAGACGCGGGGAGGACCGGGGAGAGACGAGAGACGGGAGGA	798
QY	1128	TGCTTTGGCAACGGAGAGTGTTTGTGTGAGAGATGAGAACCCACACGAAGTTGTTCGAGA	1187
Db	797	CGGGAGGACCAAGGACCGGGGAGGACCGGGGAGACGACGAGACGGGAGGACCGGGAGAGACA	738
QY	1188	GGTCCACGTGAGCACCGTGTGGAAGAACAGAGAGGAGCACAGGAGAGGAGAGAGCTGA	1247
Db	737	GGACCGGGAGGACCAAGGACCGGGGAGGACGGGGAGGACGAGACGAGACGCGGAGAGCGG	678
QY	1248	AGGGGGCGTGGTGTAGAAAGAACAGGAGAAATCCTTGCCCTCGAACAATCGGTGAGGC	1307
Db	677	GGAGGACCGGGAGGAGGACGAGGACCGGGGAGGACGAGAGCGGGGAGGACGGGAGAGACGG	618
QY	1308	CCAGAGAGTCCCCAGCAAGACTGAGCCTGCTGAGAGAGCTGATGAAGACAGAGAGATGTG	1367
Db	617	GGAGGACGAGGACCGGGGAGGAGGACGAGGACCGGGGAGGACCGGGGAGGAGGAGGA	558
QY	1368	TGTCTCTGAGGAGAC	1383
Db	557	CGAGGACCGGGAGGAC	542

RESULT 7
US-09-249-585A-2
; Sequence 2, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:

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: APPLICANT: Horlick, Robert
: TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
: FILE REFERENCE: 0867/OD905
: CURRENT APPLICATION NUMBER: US/09/249,585A
: CURRENT FILING DATE: 1999-02-11
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 1926
: TYPE: DNA
: ORGANISM: Epstein Barr Virus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1926)
: OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

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Query Match	1.4%;	Score 70.8;	DB 4;	Length 1926;
Best Local Similarity	45.3%;	Pred. No. 4.8e-08;		
Matches 335; Conservative	0;	Mismatches 402;	Indels 3;	Gaps 2;

QY	914	ANAGAGTATGATCTGAAACTGCCCCGAGACAGAAAGAGACGACAAAGGCAAAAAAGTAAAGC	973
Db	333	AGGAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGG	392
QY	974	AGGAAAGAAAAGAAAACAGACAGAGCCCTCGGAGGAGCAGAGGCCGGCAGAAAGCACAG	1033
Db	393	AGCAGAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGG	452
QY	1034	ACCAAGCCAGGTTTTCAGACAGACTTACGAGAGGCTGGAGCTGCTTTGGAAGCAGGTTG	1093
Db	453	AGGAGGGCCAGAGGGGCAGAGAGCCAGAGAGGAGGGGCAGAGGGGCAGAGGGGCAGGAGC	512
QY	1094	GTGACCTGGAGGCATTCGTCAGAGAGAAAGTGTCTCTTTGGCAACGAAAGTTTGATG	1153
Db	513	AGGAGAGGGGCAGAGACAGAGAGGGGCAGAGGGGCAGAGAGCAGACAGAGAGGGGCAGG	572
QY	1154	AGAAGATGAAGCCACCACCAAGATTGTTTCAAGCTCCACCTGAGACCCGTGAGAGA	1213
Db	573	AGGGCAGAGGGGCAGAGACAGAGAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGG	632
QY	1214	CAGAGGAGAGCAGGAGGAGAGAGAGGCTTGAAAGGGGCGTGTGTGAGAGGACAG	1273
Db	633	AGGGCAGAGACGA-CGAGGGGCAGAGACAGAGAGAGGGGCAGAGAGGGGCAGAGGGGCAG	691
QY	1274	GAGAACTCTTCCCCCTGAGAAACTGGCTGTAGCCCCAGAGGTCCCCCAAGSAACTGTAGC	1333
Db	692	GAGCA--GGAGGGGCAGAGAGAGAGGGGCAGAGAGGGGCAGAGGGGCAGAGGGGCAG	749
QY	1334	CTGCTGAGAGACCTGATGAGAGCAGAGACATGTGTCTCTGTGAGAGACCACTCTAAC	1393
Db	750	AGGAGGGGCAGGAGACAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGG	809
QY	1394	TGCAGACCTTAAGTCTGGAAGAGAGCGCTGCCAAACACCAGAGGGCATTTGCAATG	1453
Db	810	AGCAGAGAGAGGGGCAGAGAGGGGCAGAGAGCAGAGAGGGGCAGAGGGGCAGAGGACG	869
QY	1454	AGGTGGAGATCTCTCTCTCAGGAAAGATCAAGTAAAGGGAAGTCCCTTGAAGAAAC	1513
Db	870	AGGGCAGAGAGGGGCAGAGACAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGGG	929
QY	1514	TCTTCAGTACCTCAGGCTTAAAGACAGCTGTCTGGAAAGACAGAAAGGGGAAACAGAGAG	1573
Db	930	GGCAGGAGCAGGAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGAGGG	989
QY	1574	GTGGGAGAGAGAGAGCTTGAGAAATACCAACATTCATTCACACCGAATCCCGAGAGATG	1633
Db	990	TGAGAGAGAGCGTGAAGCGGGGTGAGAGAGTAACTGAGAGCCGGGTTCAGAGAGGTAG	1049
QY	1634	CTGATGAGCAGAGGAGAG	1653
Db	1050	TGGAAGCCCGCGGGGTAGAG	1069


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QY 1034 ACCAGCCAGGTTGTCACGACTACGAGAAAGTGAGCTCCCTTTGGAAGACGAGTTG 1093
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 882 AGGAGGGGACGAGAGGCGCAGAGGCGCAGAGGGCGCAGAGGGCGCAGAGG 941
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1094 GTGACCTTGAGGACATCGTCAGAGGAAGTGTGCTCTTTGGCAACGGAAGTGTGATG 1153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 942 AGGAGGAGGGGCGAGAGCAGAGAGGGGCGAGAGGGGCGAGAGGAGGAGGGGCGAGG 1001
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1154 AGAGATGGAAGCCACCAAGAAATTGTCAGAGCTCCAGCTGAGCACCCTGAGAGA 1213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1002 AGGGGCGAGAGGCGCAGAGCAGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAGG 1061
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1214 CAGAGGAGCAGAGGAGAGAGAGAGCTGAAGGGGCGCTGGTGTAGAAGAGACAG 1273
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1062 AGGGGCGAGAGCA-GGAGGGGCGAGAGCAGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAG 1120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1274 GAGAACTCTTCCCCCTGAGAACTGCTGAGCCCGCAGAGAGTCCCGCAGGAAGCTGAGC 1333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1121 GAGCA--GGAGGGGCGAGAGCAGAGAGGGGCGAGAGGCGCAGAGAGGAGGAGG 1178
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1334 CTGCTGAGAGAGCTGATGAAGACAGAGAGATGTGTCTCTGAGAGAGCCACTCAAC 1393
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1179 AGGAGGGGCGAGAGCAGAGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAGG 1238
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1394 TGACAGACCTAAGTCTGAAGAGAACGCTGCCCAACACCCAGAGAGGCAATTGTCACTG 1453
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1239 AGCAGAGAGAGGGGCGAGAGGGGCGAGAGAGAGAGGGGCGAGAGGGGCGAGAGGAGG 1298
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1434 AGGTGAAGTGTCTCTCTCTGAGAAAGATCAAGTACAGGGAAGTCCCTTGAAGAAAC 1513
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1299 AGGGGCGAGAGGGGCGAGAGGAGGGGCGAGAGGGGCGAGAGGAGGGGCGAGAGG 1358
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1514 TCTTCAGTAGCTCAGCAAGCTTTAAAGAGCTGTCTGAGAGAGCAGAGAGGGGAAACGAGAG 1573
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1359 GGCAGAGAGCAGAGAGAGGGGCGAGAGGCGCAGAGAGGCGCAGAGAGGAGGAGGCGGGG 1418
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1574 GTGGGAGAGCAGAGAGCTGTGAGAAATACCAACATTTCACCCGAAATCCCGAGAGATG 1633
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1419 TCGAGAGGCACTGTAGAGGCGGGGTCTGAGAGTAGTGTGAGGCGGGGTCTGAGAGAGTAG 1478
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1634 CTGATGAGCAGAGAGGAGAG 1653
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1479 TCGAGGCGCGCGGGGTAGAG 1498
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 755.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-884-811-15

Query Match
Best Local Similarity: 45.3%, Pred. No. 1.1e-07;
Matches 335; Conservative 0; Mismatches 402; Indels 3; Gaps 2;

QY 914 AAGAGATGATCTGTGAACCTCCGAGAAAGAGAGAGCAGCAAGAGGCAAGAAAGTACAGC 973
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2296 AGGAGGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAGG 2355
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 974 AGGAAGAAAGGAAAGACAGAGCCAGCTCGAGAGCAGAGAGGCGCAGAGAGGCGCAGAGAG 1033
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2356 AGCAGAGAGAGGGCGCAGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGAGGAGGCGCAGAG 2415
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1034 ACCAGGCGAGGTTGTCCACAGACTACGAGAAAGTGAGCTCCCTTTGGAAGACAGGTTG 1093
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2416 AGGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGCGCAGAGAGGGGCGAGAGGGGCGAGAGC 2475
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1094 GTGACCTTGAGGACATGTGACAGAGAAAGTGTCTCTTTGGCAACGGAAGTGTGATG 1153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2476 AGGAGAGAGGGGCGAGAGCAGAGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGAGGGGCGAGG 2535
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1154 AGAAGATGAAGCCCAACCAAGAAAGTTGTCAGAGTGTCTGAGAGAGCCAGCGAGAGAGA 1213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2536 AGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAGAGGCGAGG 2595
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1214 CAGAGAGAGCAGAGGAGAGAGAGAGGCTGAAGGGGCGCTGGTGTAGAAGGAGACAG 1273
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2596 AGGGGCGAGAGGCGCAGAGGCGCAGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGCGAGG 2654
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1274 GAGAACTCTTCCCCCTGAGAAACTGCTGAGCCCGCAGAGAGTCCCGCAGGAAGCTGAGC 1333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2655 GAGCA--GGAGGGGCGAGAGCAGAGAGGGGCGAGAGGCGCAGAGAGGCGAGAGGAGG 2712
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1334 CTGCTGAGAGAGCTGATGAAGACAGAGAGATGTGTCTCTGAGAGAGCCACTCAAC 1393
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2713 AGGAGGGGCGAGAGCAGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGGGCGAGAGG 2772
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1394 TGACAGACCTAAGTCTCTGAAGAGAGAGCTGCCCAACACCCAGAGAGCAATTGTCACTG 1453
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2773 AGCAGAGAGAGGGGCGAGAGGGGCGAGAGGCGCAGAGAGGAGGAGGAGGCGAGAGGAGG 2832
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1454 AGGTGAAGTGTCTGTCTCTCAGGAAGATCAAGTACAGGGAAGTCCCTTGAAGAAAC 1513
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2833 AGGGGCGAGAGGGGCGAGAGGAGGGGCGAGAGGGGCGAGAGGAGGAGGAGGAGG 2892
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1514 TCTTCAGTAGCTCAGGCTTTAAAGAAAGCTGTCTGGAAGAGCAGAGAGGGGAAACAGAGAG 1573
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2893 GGCAGAGCAGAGAGAGGGGCGAGAGGCGCAGAGAGGCGCAGAGAGGAGGAGGAGGCGGGG 2952
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1574 GTGGGAGAGCAGAGAGCTGTGAGAAATACCAACATTTCACCCGAAATCCCGAGAGATG 1633
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2953 TCGAGAGGCACTGTAGAGCGGGGTCTGAGAGTAGTGTGAGGCGGGGTCTGAGAGAGTAG 3012
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1634 CTGATGAGCAGAGAGGAGAG 1653
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3013 TCGAGGCGCGCGGGGTAGAG 3032
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 14

Best Local Similarity 45.3%; Pred. No. 1.1e-07;
Matches 335; Conservative 0; Mismatches 402; Indels 3; Gaps 2;

```
OY 914 AAGAGATATCTGGAACTGCCGAGAAAGAGCAAGAGGCGCAAAAAGTAGACG 973
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2296 AGGAGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGG 2355
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 974 AGGAGAAAAGGAAAAGACAGAGCCCTCGGAGGAGCGAGAGCCGCGCAAGAACACAG 1033
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2356 AGCAGAGAGAGGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGG 2415
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1034 ACCAGGCCAGGTTGTCAGAGACTACAGAGGTGAGCTGCCCTTTGAAAGACAGTTG 1093
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2416 AGGAGGGGCGAGAGGGGCGAGAGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGGAGC 2475
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1094 GTGACCTGAGGCTATGCTCAGAGAGAAAGTGTCTCTTTGCAACGAAAGTTTGATG 1153
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2476 AGGAGAGAGGGGCGAGAGAGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGG 2535
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1154 AGAAGATGGAAGCCCAACAAGATTGTTGACAGAGGTCCACGTGAGCACCCTGAGAGA 1213
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2536 AGGGGCGAGAGGGGCGAGAGCGAGAGAGGGGCGAGAGCGAGAGGGGCGAGAGGGGCGAGG 2595
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1214 CAGAGAGGAGCAGGAGGAGAGAGAGGCTGAAAGGGGCGTGTGTGTAAGAAAGACAG 1273
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2596 AGGGGCGAGAGCA -GGAGGGGCGAGAGCAAGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGG 2654
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1274 GAGAAATCTTGGCCCCCTGAGAAATCTGTAGCCCCAGAGGTCCCCCAGAGAGCTGAGC 1333
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2655 GAGCA--GGAGGGGCGAGAGGAGAGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCG 2712
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1334 CTGCTGAGGAGCTGATGAGAGCAGAGATGTGTCTCTGTGAGAGAGACCACTCAAC 1393
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2713 AGGAGGGGCGAGAGCGAGAGGGGCGAGAGGGGCGAGAGCGAGAGGGGCGAGAGGGGCGAGG 2772
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1394 TGACAGACCTAAGTCTCTGAAGAGAGACGCTGCCCAACACCAGAAAGGCATTGTCAATG 1453
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2773 AGCAGAGAGAGGGGCGAGAGGGGCGAGAGCGAGAGAGGGGCGAGAGGGGCGAGAGGACAGG 2832
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1454 AGGTGAGATGCTGTCTCTCAGGAAAGAAATCAAGGTACAGGGAAGTCCCTTGAGAAAC 1513
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2833 AGGGGCGAGAGGGGCGAGAGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGG 2892
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1514 TCTTCAGTAGCTCAGGCTTAAGAAAGCTGTGGAAGAAAGCAGAAAGGGAAACGAGAGAG 1573
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2893 GGCAGAGAGCAGAGAGGGGCGAGAGCGAGAGGGGCGAGAGGGGCGAGAGGGGCGAGAGGGGCG 2952
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1574 GTGGGGAGACGACAGACCTTGAAGAAATACCAACATTCAACCGAATCCCCAGAGAGTg 1633
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2953 TCGAGAGGCGAGTGGAGCCGGGTGAGAGGTAGTGGAGGCCGGGCTCGAGAGAGTgAG 3012
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1634 CTGATGAGCAGAAAGGAGAG 1653
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3013 TGGAGGCCCGCGGGGTAGAG 3032
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: December 9, 2002, 21:27:54
Job time : 297 secs

Db	213	GTCAAGGGCTACTTAACACAGAGATGTCTCATTCAGAGGAAAACAGAGGGGAC	272
Qy	241	GAGGAGAAATCTCCTTATGATGATGTGGACGACAGATCAGAAGATGTGAGAAAA	300
Db	273	GAGGAAACATCTGTATGATGAGATGTGTGACAGCGACAGATCAGAAAGATGTAGAAAA	332
Qy	301	GACCGATTAAGAAATGGCGGCCAACTCCACACTGTTTGAAGATATACAAAGATGG	360
Db	333	GACCGATTTAAATAATGGCGGCCAACTCCACACTGTTTGAAGATATACAAAGATGG	392
Qy	361	CAGGAGAGACATCAGAAATTAATTGAACAGATCCCTGCTTCAGAAAACAATGTGAGAA	420
Db	393	CAGGAGAGACATCAGAAATTAATTGAACAGATCCCTGCTTCAGAAAACAATGTGAGAA	452
Qy	421	ATGATACAGCTGCTGAGTCCAGGCTTAATGATGTGTGCTTCAAGAAATTTAAATTT	480
Db	453	ATGATACAGCTGCTGAGTCCAGGCTTAATGATGTGTGCTTCAAGAAATTTAAATTT	512
Qy	481	GTTGCTTTTAAATTCACGCTGAAGAAGATTAATAATGAATACTAGATCTGTCCACTA	540
Db	513	GTTGCTTTTAAATTCACGCTGAAGAAGATTAATAATGAATACTAGATCTGTCCACTA	572
Qy	541	CTCACTGTCAAGAAAGATGAAGGCGAAGGGGCGAAGGCTGTGTGAGCTGTGAGACAC	600
Db	573	CTCACTGTCAAGAAAGATGAAGGCGAAGGGGCGAAGGCTGTGTGAGCTGTGAGACAC	632
Qy	601	CAGAGCCCAAGTGTGAGACTGCGCTGCGAGATCAGATCCCAAGAAATGAGCTGAG	660
Db	633	CAGAGCCCAAGTGTGAGACTGCGCTGCGAGATCAGATCCCAAGAAATGAGCTGAG	692
Qy	661	CAATCCACAGAGAAACAAGAGCCACCTGTAAACAAGACAGACACAGAAATCCC	720
Db	693	CAATCCACAGAGAAACAAGAGAGCCACCTGTAAACAAGACAGACACAGAAATCCC	752
Qy	721	CTTCAAGCCGAATGTGATCTCAGGCGCTGAGGAAAGAACCAAGATGAAGGAGAAATAA	780
Db	753	CTTCAAGCCGAATGTGATCTCAGGCGCTGAGGAAAGAACCAAGATGAAGGAGAAATAA	812
Qy	781	CAAGAGAAAGAGCCACCAAGTCCCAAGATCCCGAGAGCCCAAGTACAGTGTAGACA	840
Db	813	CAAGAGAAAGAGCCACCAAGTCCCAAGATCCCGAGAGCCCAAGTACAGTGTAGACA	872
Qy	841	ACATCTTCTTCAAGAGTCTTCACTCACGATGTGGGCGGCTGGCGCAAGAACCAAGC	900
Db	873	ACATCTTCTTCAAGAGTCTTCACTCACGATGTGGGCGGCTGGCGCAAGAACCAAGC	932
Qy	901	TTCAAGAAATCAAAAGAGATGTATCTGGAACCTCCGCAACAGAAAGACAGCAAGACA	960
Db	933	TTCAAGAAATCAAAAGAGATGTATCTGGAACCTCCGCAACAGAAAGACAGCAAGACA	992
Qy	961	GAAGAAAGTAGACGAGGAAGAAAGGAAGAAACACAGAGCCAGCCTCGAGAGAGCAGAGCCG	1020
Db	993	GAAGAAAGTAGACGAGGAAGAAAGGAAGAAACACAGAGCCAGCCTCGAGAGAGCAGAGCCG	1052
Qy	1021	GCAGAGACACACAGCCAGGCCAGTGTCTACAGACTACGACAAAGTGTAGCTGCTTTG	1080
Db	1053	GCAGAGACACACAGCCAGGCCAGTGTCTACAGACTACGACAAAGTGTAGCTGCTTTG	1112
Qy	1081	GAAAGCCAGTGTGGTGCCTGTGAGGCACTGTCAGAGCAACAAATGTGCTTTGGCAACG	1140
Db	1113	GAAAGCCAGTGTGGTGCCTGTGAGGCACTGTCAGAGCAACAAATGTGCTTTGGCAACG	1172
Qy	1141	GAAGTGTGTGATGAGATGTGAAGGCCACACAGAGTGTGTGACAGAGTCCACTGTAGC	1200
Db	1173	GAAGTGTGTGATGAGATGTGAAGGCCACACAGAGTGTGTGACAGAGTCCACTGTAGC	1232
Qy	1201	ACCGTGAAGACACAGAGGAGGACAGGAGAGGAGAGGAGAGGCTGAAGGGGCGTGTG	1260
Db	1233	ACCGTGAAGACACAGAGGAGGAGGAGGAGGAGGAGAGGCTGAAGGGGCGTGTG	1292
Qy	1261	GTAGAGGACAGAGAAATCTTGTCCCTCTGAGAACTGGCTGAGCCCAAGAGTCCCC	1320

Db	1293	GTAAAGAACACAGAGAAATCTTGGCCCTTGAGAAACTGCTGAGAGCCCGAGAGTCC	1352
Qy	1321	CAGGAACTGAGCCTGCTGAGAGACTGATGAAGACAGAGATGCTGTCTGAGGA	1380
Db	1353	CAGGAGCTGAGCCTGCTGAGAGCTGATGAAGACAGAGATGTGTCTTGAGGA	1412
Qy	1381	GACCACTCAACTGACACACTTAATCTCTGAAGAAAGCGTGGCCCAACCCGAA	1440
Db	1413	GACCACTCAACTGACACACTTAATCTCTGAAGAAAGCGTGGCCCAACCCGAA	1472
Qy	1441	GCAATGTCACTGAGTGGAGTATGCTGTCTCTCAAGAAAGTAATCAAGTACAGGAAGT	1500
Db	1473	GCATGTGTCACTGAGTGGAGTATGCTGTCTCTCAAGAAAGTAATCAAGTACAGGAAGT	1532
Qy	1501	CCCTTGAAAGAACTCTTCAGTAGCTCAGGCTTAAAGAGCTGTCTGGAGAGACAGAG	1560
Db	1533	CCCTTGAAAGAACTCTTCAGTAGCTCAGGCTTAAAGAGCTGTCTGGAGAGACAGAG	1592
Qy	1561	GGGAAACGAGAGAGTGGGGAGACGAAAGCCTGGAGATACCAACACATTCACACGAA	1620
Db	1593	GGGAAACGAGAGAGTGGGGAGACGAAAGCCTGGAGATACCAACACATTCACACGAA	1652
Qy	1621	TCCCCAGAGAGTGTGTATGAGCAAGAGGAGAGAGTGTGCTGCTCCCGAGAGAGCT	1680
Db	1653	TCCCCAGAGAGTGTGTATGAGCAAGAGGAGAGAGTGTGCTGCTCCCGAGAGAGCT	1712
Qy	1681	GAGGAGACACAGTCTGTGGAGAAAGGGCCGCTGAGACACCCAGAGATGGGAGACTGAG	1740
Db	1713	GAGGAGACACAGTCTGTGGAGAAAGGGCCGCTGAGACACCCAGAGATGGGAGACTGAG	1772
Qy	1741	GAGGAACTACTTCCGATGTGAGAGAAAGAGAGAGAGATACCTCGTGGGACCTCTC	1800
Db	1773	GAGGAACTACTTCCGATGTGAGAGAAAGAGAGAGAGATACCTCGTGGGACCTCTC	1832
Qy	1801	AAAAAGTGTGTGACACCCAGAAAGCGGCTCGAAGACTCTTGAGAGTGAACAGAGAA	1860
Db	1833	AAAAAGTGTGTGACACCCAGAAAGCGGCTCGAAGACTCTTGAGAGTGAACAGAGAA	1892
Qy	1861	GAGCTGAGAAAGTGCANAGCGCACCTTCTCTCACTGATAGCACAGTGCAGAAATG	1920
Db	1893	GAGCTGAGAAAGTGCANAGCGCACCTTCTCTCACTGATAGCACAGTGCAGAAATG	1952
Qy	1921	CAGAGTGAAGTCAAAACCTGTGTGGAGAGAACCAACCCAGAGAACCAAGGCTAGGGTG	1980
Db	1953	CAGAGTGAAGTCAAAACCTGTGTGGAGAGAACCAACCCAGAGAACCAAGGCTAGGGTG	2012
Qy	1981	GATACTTGAAGTCTTGGGAAAGCACTGATTTGTGTGATCACTCCAGAAAGAGACAGG	2040
Db	2013	GATACTTGAAGTCTTGGGAAAGCACTGATTTGTGTGATCACTCCAGAAAGAGACAGG	2072
Qy	2041	AAGCATCTCTTTCAGTATGATGAAGAGGGCCAGAGACACTGGAGGGGACAGTACAGA	2100
Db	2073	AAGCATCTCTTTCAGTATGATGAAGAGGGCCAGAGACACTGGAGGGGACAGTACAGA	2132
Qy	2101	GCAGAGAGGCGCACAAAGACAAAGAGCCGAGAACAGAGCGTGTCTGTCCAGCACCCAG	2160
Db	2133	GCAGAGAGGCGCACAAAGACAAAGAGCCGAGAACAGAGCGTGTCTGTCCAGCACCCAG	2192
Qy	2161	GAGCAGAGCAAGAGCGCAAGAGAGTCTCTACCCGAGACCAAGCGGAGAAAGGCTTCGAAAGG	2220
Db	2193	GAGCAGAGCAAGAGCGCAAGAGAGTCTCTACCCGAGACCAAGCGGAGAAAGGCTTCGAAAGG	2252
Qy	2221	GAAGGTGTCTCACTTGGGAGTCAATTTAAAGATAGTCACTCCAGAGAAATTCAG	2280
Db	2253	GAAGGTGTCTCACTTGGGAGTCAATTTAAAGATAGTCACTCCAGAGAAATTCAG	2312
Qy	2281	TCAAAACTGGAAGAAAGCCGAAAGACTTATAGTGTAGACAGTGTGTCACTGAGATCGAA	2340
Db	2313	TCAAAACTGGAAGAAAGCCGAAAGACTTATAGTGTAGACAGTGTGTCACTGAGATCGAA	2372
Qy	2341	CGAGTAAAGAAAGATCTTGGGTTTCATTTAAAAATTCATCCCGAGAGGCGGAGAA	2400
Db	2373	CGAGTAAAGAAAGATCTTGGGTTTCATTTAAAAATTCATCCCGAGAGGCGGAGAA	2432

QY 2401 AGGCGAGAGGGAAGCAAGCAAGCCACTGTGGAAGACTCAGGGCCAGTGAGATTAAT 2460
|||||
Db 2433 AGGCGAGAGGGAAGCAAGCAAGCCACTGTGGAAGACTCAGGGCCAGTGAGATTAAT 2492
QY 2461 GAGGAGGACCTTAATGTCCAGCGCTGTGCTCTGTCTGAGTAATTAATGACGTGAGAGG 2520
|||||
Db 2493 GAGGAGGACCTTAATGTCCAGCGCTGTGCTCTGTCTGAGTAATTAATGACGTGAGAGG 2552
QY 2521 GAGAATATGGAAGCCCAAGGGGAATACGGAGCTCCCGACGTGCTGGGGCTGTGTACGTG 2580
|||||
Db 2553 GAAATATGGAAGCCCAAGGGGAATACGGAGCTCCCGACGTGCTGGGGCTGTGTACGTG 2612
QY 2581 TCCGAGAGCTCAGTAAGACTGTGTCCACACTGTGAGTATCCGACATTAATGATGGGACC 2640
|||||
Db 2613 TCCGAGAGCTCAGTAAGACTGTGTCCACACTGTGAGTATCCGACATTAATGATGGGACC 2672
QY 2641 AGGCGAGTACCAAGTGTGGAAGAGCGGTCTCTGTGTGATATCCGCTTCCGTAAAGAA 2700
|||||
Db 2673 AGGCGAGTACCAAGTGTGGAAGAGCGGTCTCTGTGTGATATCCGCTTCCGTAAAGAA 2732
QY 2701 CCTCTTGAACACACAGCGGGAAGAGCCATGCCACTGTGTAAGAGTCACTGAAAAAGAC 2760
|||||
Db 2733 CCTCTTGAACACACAGCGGGAAGAGCCATGCCACTGTGTAAGAGTCACTGAAAAAGAC 2792
QY 2761 ATCATTTGCAAGAAACTCTGTGTCTCACCCAGACGTTACAGAGGTTAAAGTCCCAT 2820
|||||
Db 2793 ATCATTTGCAAGAAACTCTGTGTCTCACCCAGACGTTACAGAGGTTAAAGTCCCAT 2852
QY 2821 GACGACATGGTCCACAGTGTGGAAGTGAATTCACCTCAGAAAGCTGTGAAGCCACAGAGACC 2880
|||||
Db 2853 GACGACATGGTCCACAGTGTGGAAGTGAATTCACCTCAGAAAGCTGTGAAGCCACAGAGACC 2912
QY 2881 TCAGAGAGCTCTCGTGTACTGAAGAGTTACCAGAGCATCGGGGGCCGAAGACACACAGAC 2940
|||||
Db 2913 TCAGAGAGCTCTCGTGTACTGAAGAGTTACCAGAGCATCGGGGGCCGAAGACACACAGAC 2972
QY 2941 ATGAGTCCGAGATTTCCAGAGTGTGACTGCCAGACACACAGAGGAGGACACCCCA 3000
|||||
Db 2973 ATGAGTCCGAGATTTCCAGAGTGTGACTGCCAGACACACAGAGGAGGACACCCCA 3032
QY 3001 GTTCAGAGGTAGAGAGTGTGTGCTAGATACAGAAAGAGAGAGGCCGACGACGAGGCC 3060
|||||
Db 3033 GTTCAGAGGTAGAGAGTGTGTGCTAGATACAGAAAGAGAGAGGCCGACGACGAGGCC 3092
QY 3061 ATCTCTCAAGCCGTTGCAACAGAGGTGAAGAGAGTCCAGAGTGCCTGCACACCCAGACT 3120
|||||
Db 3093 ATCTCTCAAGCCGTTGCAACAGAGGTGAAGAGAGTCCAGAGTGCCTGCACACCCAGACT 3152
QY 3121 GTTCAGAGAAAGGGGTCAAAAGCACTGGAAGAGTTGAGAGAGGTAGAGAGGACCTCCGAA 3180
|||||
Db 3153 GTTCAGAGAAAGGGGTCAAAAGCACTGGAAGAGTTGAGAGAGGTAGAGAGGACCTCCGAA 3212
QY 3181 GTGCTGGCTTCGAGAGAAGAGAGACGTTATGCCGAAAGAGCCGTCGACGAGAACTGGA 3240
|||||
Db 3213 GTGCTGGCTTCGAGAGAAGAGAGACGTTATGCCGAAAGAGCCGTCGACGAGAACTGGA 3272
QY 3241 GGTGACATCTTGTGCAAGGGCTGTGAGACTGGAAGAGTACTCTCCAGAGAGCTTGAAGTT 3300
|||||
Db 3273 GGTGACATCTTGTGCAAGGGCTGTGAGACTGGAAGAGTACTCTCCAGAGAGCTTGAAGTT 3332
QY 3301 CCTGAAGTACAGGAGATGTAGACATGTGCCAGCTGCCAGGTATTCAGAAAGTCCAGCAG 3360
|||||
Db 3333 CCTGAAGTACAGGAGATGTAGACATGTGCCAGCTGCCAGGTATTCAGAAAGTCCAGCAG 3392
QY 3361 CTGATGGAACAGGCGCTGAGTATCCGAAACCTTGAACAGACAGTGAACAAAT 3420
|||||
Db 3393 CTGATGGAACAGGCGCTGAGTATCCGAAACCTTGAACAGACAGTGAACAAAT 3452
QY 3421 GGAAGACACTCTTACAGATTCAGACACTGCGAGATGGGACACAGCAAGTGAACCAATT 3480
|||||
Db 3453 GGAAGACACTCTTACAGATTCAGACACTGCGAGATGGGACACAGCAAGTGAACCAATT 3512

QY 3481 GACAGCCAGACAGTAAGAGCCACTGAGCTGTGACAGGAGTCAAGAGTCAACAGAAGAG 3540
|||||
Db 3513 GACAGCCAGACAGTAAGAGCCACTGAGCTGTGACAGGAGTCAACAGAAGAGAG 3572
QY 3541 GCGGCTACTGCTCAGAAAAGAGAGCCTTGACACTACTTAATTAATGTTCCAGCCAGAA 3600
|||||
Db 3573 GCGGCTACTGCTCAGAAAAGAGAGCCTTGACACTACTTAATTAATGTTCCAGCCAGAA 3632
QY 3601 GAACATGGGGAAGAACCCAGGAAGAGATGTTCTTGAACCTTACACAGCAAGAGCTTACTGCT 3660
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Db 3633 GAACATGGGGAAGAACCCAGGAAGAGATGTTCTTGAACCTTACACAGCAAGAGCTTACTGCT 3692
QY 3661 GCAGCCGTGCGCTTGTGCGAAAGACTGAGAGTGGTCAAGAGGTTGAGGTTGCTGTTG 3720
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Db 3693 GCAGCCGTGCGCTTGTGCGAAAGACTGAGAGTGGTCAAGAGGTTGAGGTTGCTGTTG 3752
QY 3721 GATGAGAAAAAAGTCAAAAGAAAGAGAGGTTTGTACACTCTGAGCCCAACAGTCAA 3780
|||||
Db 3753 GATGAGAAAAAAGTCAAAAGAAAGAGAGGTTTGTACACTCTGAGCCCAACAGTCAA 3812
QY 3781 AAGGCTGCTGATGTGACATTTGACAGTGAAGTATGAGGAGTGGCCGGGTGTCAAGAAAAG 3840
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Db 3813 AAGGCTGCTGATGTGACATTTGACAGTGAAGTATGAGGAGTGGCCGGGTGTCAAGAAAAG 3872
QY 3841 GAGAGTACTGAAAGTGCAGAGCTTTAGCCTGGAGAGGAGAGAGATGGAACCTGACGTTGAA 3900
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Db 3873 GAGAGTACTGAAAGTGCAGAGCTTTAGCCTGGAGAGGAGAGAGATGGAACCTGACGTTGAA 3932
QY 3901 AAGGAGAAAAAGGAGACAAAGCCAGAGCAAGTGAAGAAAGTGAAGCAGCAAGAGCC 3960
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Db 3933 AAGGAGAAAAAGGAGACAAAGCCAGAGCAAGTGAAGAAAGTGAAGCAGCAAGAGCC 3992
QY 3961 GCTCTGAGCATTAAGAAACCTACGGGAAGCCAGTCTGACACTTTGACATGCCACTCA 4020
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Db 3993 GCTCTGAGCATTAAGAAACCTACGGGAAGCCAGTCTGACACTTTGACATGCCACTCA 4052
QY 4021 GAGAGGGGGAAGGACATGGGAAGCTTGGAGAGGCCCTTCTCCAGACCAAGACAAA 4080
|||||
Db 4053 GAGAGGGGGAAGGACATGGGAAGCTTGGAGAGGCCCTTCTCCAGACCAAGACAAA 4112
QY 4081 GCAGGTTGCATAGAGGTTCAAGTTCAAAGCCTGGACACAACAGTCACTCAACAGCAGAA 4140
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Db 4113 GCAGGTTGCATAGAGGTTCAAGTTCAAAGCCTGGACACAACAGTCACTCAACAGCAGAA 4172
QY 4141 GCTGTGAAAAAGTCAATAGAAAGGTTGTGATTTGACAGACAGGTAAAGTCCAGAGTGT 4200
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Db 4173 GCTGTGAAAAAGTCAATAGAAAGGTTGTGATTTGACAGACAGGTAAAGTCCAGAGTGT 4232
QY 4201 GTAGGTGCACACTTATTACAGCTGGAAGTCTCTGCAACGGGTGGCCACTGGACTTT 4260
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Db 4233 GTAGGTGCACACTTATTACAGCTGGAAGTCTCTGCAACGGGTGGCCACTGGACTTT 4292
QY 4261 CAGCATGCAAGAGACAGGTAACCCCTGGGGCCTGAGTCTCAGGACAGATTCATCCCAATC 4320
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Db 4293 CAGCATGCAAGAGACAGGTAACCCCTGGGGCCTGAGTCTCAGGACAGATTCATCCCAATC 4352
QY 4321 ATTAGTAACCTCTGCTCTGAAAGACACCTTACATCTCTGAGCTTAAGAGAAATAAAGCGCA 4380
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Db 4353 ATTAGTAACCTCTGCTCTGAAAGACACCTTACATCTCTGAGCTTAAGAGAAATAAAGCGCA 4412
QY 4381 TCCCAAGAGAGAGGATCAGAGAGAAAGAGAACCCAGATGCTGCTGATGCTGACGGC 4440
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Db 4413 TCCCAAGAGAGAGGATCAGAGAGAAAGAGAACCCAGATGCTGCTGATGCTGACGGC 4472
QY 4441 AAGGAGATACAGCAATCGAAAAAGTCTCAAGGCTGAACCTGAGATCTCTGAACTTGAAG 4500
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Db 4473 AAGGAGATACAGCAATCGAAAAAGTCTCAAGGCTGAACCTGAGATCTCTGAACTTGAAG 4532
QY 4501 AGTAAAGCAACAAGATTTGTGCTGAACGTCATTTCAACAGCCGTTACCAAGTTCGACGCT 4560
|||||
Db 4533 AGTAAAGCAACAAGATTTGTGCTGAACGTCATTTCAACAGCCGTTACCAAGTTCGACGCT 4592
QY 4561 ACAGAAACAGCCCCGAAACTCATGCTTATGATTCACAGACCCAGGTCTCTGATCAAGG 4620

|||||
Db 4593 ACAGAAACGCCGCCAACTCATGTTATGATTCACAGACCAGCTTCCTGCATCAG 4652
Qy 4621 CTTGACAGAGGAGGCCCAAGATGCTGACAAAAAATGAAGATCCCAAGATGAACAC 4680
Db 4653 CTTGACAGAGGAGGCCCAAGATGCTGACAAAAAATGAAGATCCCAAGATGAACAC 4712
Qy 4681 CCAGTCCCGCAGCCAGAGAGATGTCAGATCTCTGAGGCGATGGGCTCAG 4740
Db 4713 CCAGTCCCGCAGCCAGAGAGATGTCAGATCTCTGAGGCGATGGGCTCAG 4772
Qy 4741 CCTCGAAATGCTGCGGCTTGCAGTTGAAAGCCCGGTGCAAGTAAGATGAGCA 4800
Db 4773 CCTCGAAATGCTGCGGCTTGCAGTTGAAAGCCCGGTGCAAGTAAGATGAGCA 4832
Qy 4801 ACCTGCTCTCTCAACCCAAAGATCCAAAAGAGCATGCTGATGGCCCTCAGTCCAA 4860
Db 4833 AGCTGCTCTCTCAACCCAAAGATCCAAAAGAGCATGCTGATGGCCCTCAGTCCAA 4892
Qy 4861 AGCTTAGCCAGGAGGAGGCGAGTGCCTCTGAAACCTTAACCAAGATCCCGACACC 4920
Db 4893 AGCTTAGCCAGGAGGAGGCGAGTGCCTCTGAAACCTTAACCAAGATCCCGACACC 4952
Qy 4921 AACGGACCAAGCTAACCCAGAGAGGCGATCCCCCAAAGTTGAGTCCAGAGAAAGAA 4980
Db 4953 AACGGACCAAGCTAACCCAGAGAGGCGATCCCCCAAAGTTGAGTCCAGAGAAAGAA 5012
Qy 4981 ATGTACACCAAGTCACTAAAGAACAGGCCAGGAGAGAGAGAGAGAGAGAGAGAGAG 5040
Db 5013 ATGTACACCAAGTCACTAAAGAACAGGCCAGGAGAGAGAGAGAGAGAGAGAGAGAG 5072
Qy 5041 AAGGAGACCTGGCAGATCTTAAGATGTTAGTGTCTCATTTGTACTCTGTAAAGACCA 5100
Db 5073 AAGGAGACCTGGCAGATCTTAAGATGTTAGTGTCTCATTTGTACTCTGTAAAGACCA 5132
Qy 5101 ATGTGAAACCAAGTCACTAAAGAACAGAGTGTGCTGTGGAGACCTTGACCAATTTTCA 5160
Db 5133 ATGTGAAACCAAGTCACTAAAGAACAGAGTGTGCTGTGGAGACCTTGACCAATTTTCA 5192
Qy 5161 AGCCCATGAGATCCAGAGAGAGGCGGCTCAATGATTTTC 5200
Db 5193 AGCCCATGAGATCCAGAGAGAGGCGGCTCAATGATTTTC 5232

RESULT 2
US-09-902-432-1
; Sequence 1, Application US/09902432
; Patent No. US20020160002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; APPLICANT: Susan G. Jaken
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A3058-A-FMC-A 070156, 0597
; CURRENT APPLICATION NUMBER: US/09/902,432
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5134
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-902-432-1

Query Match 75.1% Score 3903.4: DB 9: Length 5134:
Best Local Similarity 97.5% Pred. No. 0:
Matches 4120; Conservative 0; Mismatches 76; Indels 31; Gaps 14;

Qy 984 GGAAGAGACAGAGCCACTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
Db 1 GGAAGAGACAGAGCCAGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Qy 1044 GTTGTAGACAGACTACGAGAGAGTGAAGTGTGCTTTGGAAAGACAGAGTGTGACTTGA 1103
Db 61 GTTGTAGACAGACTACGAGAGAGTGAAGTGTGCTTTGGAAAGACAGAGTGTGACTTGA 120
Qy 1104 GGCATGCTCAGAGAGAGAGAGTGTGCTTTGGCAACGAGAGTGTGATGAGAGATGGA 1163
Db 121 GGCATGCTCAGAGAGAGAGAGTGTGCTTTGGCAACGAGAGTGTGATGAGAGATGGA 180
Qy 1164 AGCCCAACCAAGAGTGTGTCAGAGAGTCCAGTGAACCTGTGAGAGAGAGAGAGAGAG 1223
Db 181 AGCCCAACCAAGAGTGTGTCAGAGAGTCCAGTGAACCTGTGAGAGAGAGAGAGAGAG 240
Qy 1224 GCAGGAGAGAGAGAGAGAGTGAAGGGGCGGTGTGAGAGAGAGAGAGAGAGAGAGAG 1283
Db 241 GCAGGAGAGAGAGAGAGAGTGAAGGGGCGGTGTGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 1284 GCCCCTTGAGAAACTGTGAG 1343
Db 301 GCCCCTTGAGAAACTGTGAG 360
Qy 1344 GCTGATGAAGAGCAGAGAGATGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403
Db 361 GCTGATGAAGAGCAGAGAGATGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 1404 AGTCTGAAAG 1463
Db 421 AGTCTGAAAG 480
Qy 1464 GCTGTCTCTCAG 1523
Db 481 GCTGTCTCTCAG 540
Qy 1524 CTCAGCTTAAG 1583
Db 541 CTCAGCTTAAG 600
Qy 1584 CGAAG 1643
Db 601 CGAAG 660
Qy 1644 GAAGGAG 1703
Db 661 GAAGGAG 720
Qy 1704 AGGCGCTGGAAG 1763
Db 721 AGGCGCTGGAAG 775
Qy 1764 GAAGAAG 1823
Db 776 GAAGAAG 835
Qy 1824 ACAGGCTCCAG 1883
Db 836 AC-GTCCAG 894
Qy 1884 CACCTTGTCTCAG 1943
Db 895 CACCTTGTCTCAG 954
Qy 1944 TGAGGAACAAAG 2003
Db 955 TGAGGAACAAAG 1014
Qy 2004 ACTGATTTGTGTCAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063
Db 1015 ACTGATTTGTGTCAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1071
Qy 2064 AGGAGGCGCAAG 2122

Db	1072	AAGAGGCCCAAGGACCTGGGAGGGGGACGTACAGACGAGGGGGCCACCAAGACA	11311
Qy	2123	AAGAAGCCGGAACAGACGCTGTTCTGCGACGCCAGAGACAGACCAAGCGCAAGAA	2182
Db	1132	AAGAAACC - GAAACAGAGCGTGTTCCTCCAGCACCCAGAGACAGACCAAGCGCAAGAA	1190
Qy	2183	GTTCTCAACCCGACCGACGGGAAGCCCTTCGAAAGGGAAGGTGTCTCCACTTGGAGT	2242
Db	1191	GTTCTCTACCCGACCCAGCGGAAGCCCTTCGAAAGGGAAGGTGTCTCCACTTGGAGT	1250
Qy	2243	CATTAAAAAGTTGTGACCTCCAAAGAAAAATCCAGTCAAAATCTGGAAGAAAGCCG	2302
Db	1251	CATTAAAAAGTTGTGACCTCCAAAGAAAAATCCAGTCAAAATCTGGAAGAAAGAAAG	1310
Qy	2303	AAGACTAGTGTAGAG - - - - - CAGTGTCCACTGAGATGCAACCCAGTAGAGAGA	2354
Db	1311	CCGGAAGGACCTGTGTTGTGTAGAGACAGGTTGTCTCACTGAGATGCAACCGTGTAGAA	1370
Qy	2355	ATCTTGGGTTCCATTAAGAATTCATCCCGGACGGCGGAAGAAAAAGGCGAGCGGA	2414
Db	1371	ATCTTGGGTTCCATTAAGAATTCATCCCGGACGGCGGAAGAAAAAGGCGAGTGGAA	1430
Qy	2415	- GCAAGAACCAAGCCACTGTGTGGAAGACTCAAGGCCATGAGATAAATGAGACGACCTA	2473
Db	1431	GGCAAGAACCAAGCCACTGTGTGGAAGACTCAAGGCCATGAGATAAATGAGACGACCTG	1490
Qy	2474	ATGTCCAGACCGCTGTGCTCTGTGCTGAGATTAATCACTGGGAGGGCGAAGATGAGAG	2533
Db	1491	ATGTCCAGACCGCTGTGCTCTGTGCTGAGATTAATCACTGGAGAGGAGAAATGAGAG	1550
Qy	2534	CCCAAGGGAATACGAGACTCCCCAGCTGCTGGGGCTGTACGTGTCGAGAGACTCA	2593
Db	1551	CCCAAGGGAATACGAGACTCCCCAGCTGCTGGGGCTGTGT - - - AGTGTCCGAGAGCTCA	1607
Qy	2594	GTAAGACTGTGTCACACTGTGATGTGCGACTATTATGTGGACCAAGGCGACTACCA	2653
Db	1608	GTAAGACTGTGTCACACTGTGATGTGCGACTATTATGTGGAGCACCAAGGCGACTACCA	1667
Qy	2654	GTGTGGAAGACGGGTCTCTGCGGATATCCGCTTCGTAACAGACCTCTTGAACCA	2713
Db	1668	GTGTGGAAGACGGGTCTCTCTGCGGATATCCGCTTCGTAACAGACCTCTTGAACCA	1727
Qy	2714	CAGGGGGAAGCCATGCCACTGTTGAAGAGTCACTAAAAAAGACATCATTTGAGAG	2773
Db	1728	CAGGGGGAAGCCATGCCACTGTTGAAGAGTCACTAAAAAAGACATCATTTGAGAG	1787
Qy	2774	AAACTCTGTGTACCCACAAGCTTACAGAGGGTTAAGATGCCATGACGACATGTCA	2833
Db	1788	AAACTCTGTGTACCCACAAGCTTACAGAGGGTTAAGATGCCATGACGACATGTCA	1847
Qy	2834	CCAGTGAAGTGATTTACCTCGAAGCGTGTGACCCACAAGACCTCAGAGGCTCTCC	2893
Db	1848	CCAGTGAAGTGATTTACCTCGAAGCGTGTGACCCACAAGACCTCAGAGGCTCTCC	1907
Qy	2894	GTACTGAAGATTACCGAAGCATCGGGGGCCGAAGAGCCACAGACATGTGTCCGAG	2953
Db	1908	GTACTGAAGATTACCGAAGCATCGGGGGCCGAAGAGCCACAGACATGTGTCCGAG	1967
Qy	2954	TTTCCCAAGCTGACTGCTCCCGACACACACAGAGAGCCACCCAGTTCAGAGGTAG	3013
Db	1968	TTTCCCAAGCTGACTGCTCCCGACACACACAGAGAGCCACCCAGTTCAGAGGTAG	2027
Qy	3014	AGAGTGGGTGTGATGATACGAAAGAGAGAGAGCGCCAGACGAGGACCATCTCCAAAGCG	3073
Db	2028	AGAGTGGGTGTGATGATACGAAAGAGAGAGAGCGCCAGACGAGGACCATCTCCAAAGCG	2087
Qy	3074	TTTGACAGCAAGGTGAAGAGAGATCCAGGTGCTCTCAACCCAGACTGTGCAGAGACGG	3133
Db	2088	TTTGACAGCAAGGTGAAGAGAGATCCAGGTGCTCTCAACCCAGACTGTGCAGAGACGG	2147
Qy	3134	GGTCAAAAAGCATGTGAGAGAGTTGAGAGGTAGAGGAGCTCCGAAGTGTGCTTGG	3193

Db	2148	GGTAAAGACACTGGAGACAGGTTGAGAGGTAGAGAGACTCCGATGCTGCTTGG	2207
QY	3194	AGAAAGGAGAGAGACTGTAATCCGAAAGGAGACCCGTGCAGAGACCTGGAGCTGAGACTCTTG	3253
Db	2208	AGAAAGAGAAAGACGTTATATCCGAAAGGAGACCCGTGCAGAGACCTGGAGACTGAGACTCTTG	2267
QY	3254	CACAGGCTCTGAGACTGGAAGGCTACTCCAGAGAGCCTTGAAGTCCCTGAAGTCAAGG	3313
Db	2268	CACAGGCTCTGAGACTGGAAGGCTACTCCAGAGAGCCTTGAAGTCCCTGAAGTCAAGG	2327
QY	3314	CAGATGTAGACACTGTGCGCCAGCTGGCAGGTTATCAAGTCCAGACGCTGATGGAAACAGG	3373
Db	2328	CAGATGTAGACACTGTGCGCCAGCTGGCAGGTTATCAAGTCCAGACGCTGATGGAAACAGG	2387
QY	3374	CCGTGGCCCTTGAGTCACTCCGAAACCTTGCAGACAGTGAACAATGGAAAGCACTCCCT	3433
Db	2388	CCGTGGCCCTTGAGTCACTCCGAAACCTTGCAGACAGTGAACAATGGAAAGCACTCCCT	2447
QY	3434	TAGCAGATTGACACACTGTCAGATGGGACACAGCAGAGATGAAACATTGACACCGACAGACA	3493
Db	2448	TAGCAGATTGACACACTGTCAGATGGGACACAGCAGAGATGAAACATTGACACCGACAGACA	2507
QY	3494	GTTAAAGCCACTGCAAGCTGTAGAGCACTCACAGGTCAACAAAGAAAGCGGCTACTGCTC	3553
Db	2508	GTTAAAGCCACTGCAAGCTGTAGAGCACTCACAGGTCAACAAAGAAAGCGGCTACTGCTC	2567
QY	3554	AGAAAGAGGAGCCCTTGACACTACCTAATAAATGTTCCACCCAGAGAAACACTGGGAGAG	3613
Db	2568	AGAAAGAGGAGCCCTTGACACTACCTAATAAATGTTCCACCCAGAGAAACACTGGGAGAG	2627
QY	3614	AACCAAGAAAGATGTTCTTGAACCTACACAGCAAGAGCTTACTGCTCAGCCGTGCCG	3673
Db	2628	AACCAAGAAAGATGTTCTTGAACCTACACAGCAAGAGCTTACTGCTCAGCCGTGCCG	2687
QY	3674	TTCTGCGAAAGACTGAGGTGGTCAAGAGGGTGAGTTGACTGTTGGATGGAGAAAAG	3733
Db	2688	TTCTGCGAAAGACTGAGGTGGTCAAGAGGGTGAGTTGACTGTTGGATGGAGAAAAG	2747
QY	3734	TTCAGAAAGAAACAGGAGGTGTTGTACCTGTGACGCCCAACAGTCAAAAAGCTGCTGTG	3793
Db	2748	TTCAGAAAGAAACAGGAGGTGTTGTACCTGTGACGCCCAACAGTCAAAAAGCTGCTGTG	2807
QY	3794	TGACATATGACAGTGAAGTATGGAGTGGCGGGGTGTAGAGAAAGAGAGTACTGAG	3853
Db	2808	TGACATATGACAGTGAAGTATGGAGTGGCGGGGTGTAGAGAAAGAGAGTACTGAG	2867
QY	3854	TGCAAGACTCTTAAGCTCTGGAGAGGAGAGATGGAACCTGACTTAAGAAAGAGAAAGG	3913
Db	2868	TGCAAGACTCTTAAGCTCTGGAGAGGAGAGATGGAACCTGACTTAAGAAAGAGAAAGG	2927
QY	3914	AGCAAAAGCCAGAGCAAGTAGTGAAGAGGTGAGAGGAACACCGCTCTGACGATG	3973
Db	2928	AGCAAAAGCCAGAGCAAGTAGTGAAGAGGTGAGAGGAACACCGCTCTGACGATG	2987
QY	3974	AAGGAACTTACGCGGAAGCCAGTCTTACACTTTGACATGCCACAGTCAAGAGAGGGGAGG	4033
Db	2988	AAGGAACTTACGCGGAAGCCAGTCTTACACTTTGACATGCCACAGTCAAGAGAGGGGAGG	3047
QY	4034	CACCTGGGAAGCCTTGGAGAGAGCCCTTCTCTCCAGACCAAGACAGAGGTTGCATAG	4093
Db	3048	CACCTGGGAAGCCTTGGAGAGAGCCCTTCTCTCCAGACCAAGACAGAGGTTGCATAG	3107
QY	4094	AGGTTCAAGTTCAAAGCCTGGACACAAACAGTCACTCAACACACACAACTGTGAAAAAG	4153
Db	3108	AGGTTCAAGTTCAAAGCCTGGACACAAACAGTCACTCAACACACAACTGTGAAAAAG	3167
QY	4154	TCATAGAAAGCGTTGTGATTTCAAGACACAGTGAAGTCCAGAGTGTAGGTGACACT	4213
Db	3168	TCATAGAAAGCGTTGTGATTTCAAGACACAGTGAAGTCCAGAGTGTAGGTGACACT	3227
QY	4214	TATTACCACTGAGAAAGTCCCTCTCAACGGGTGGCCACTGCACTTTCAGCATGCAGAG	4273
Db	3228	TATTACCACTGAGAAAGTCCCTCTCAACGGGTGGCCACTGCACTTTCAGCATGCAGAG	3287

OY	667	ACGAGAAAGCAAGAAAGCCACCCTGTAAGCAAGAACAGACGACACAGAAATCCCTCTTAA	726
Db	703	ACAGAGAAACCCGAAAGAGACCTTGAAGCGTGAACCAAGCACAGAAATTTCTCCCCA	762
OY	727	GCCGAAATCTGATCAAGAGGGCTGAGAGAAAGCCAAAGATGAAGGAGAAAGAAACAAG	786
Db	753	GCCGAAATCTGGCCAA---GCAGTGGAGGAATGCAAGAGAGAAAGAGAAAGCAAGAA	819
OY	787	AAAGAGCCACACAAAGTCCCGCAAGATCCCGAGCAGCCAGTCAACAGTGAACACATCT	846
Db	820	AAAGACCTTGACAAAGTGTGCAGAAATCTCGAGACTAGTCCCGTACCAGGTGAACACAGATCA	879
OY	847	TCCTTCAAGAAATTCTTCACTCACGGTTGGGCGGCTGCGCAAGAAAGCACGTTTCAAG	906
Db	880	ACCTTCAAAAATTCCTTCACTCAAGGTTGGGCGCGCTGGCCGCAAAAAGCACGTTTCAAG	939
OY	907	AAATCAAAAAGGATGATCTGGAAGTGGCGGAGAAAGAAAGAAAGCAAGAGGCAAGGCA	966
Db	940	AAAGCCGAAGGGGATGGAAGTGGAAAGCTCAGAGAAAGAAAGAAAGCAAGAGCCAG	999
OY	967	GTAGACGAGGAGAAAAGAAAAGACAGACCCAGCTCCGAGAG-----	1010
Db	1000	GTAGACACAGAAAGAAAGAGCGAAAGGACAGAGTTGCTCCGAGAAACTGACCCCTCCGAG	1059
OY	1011	-----GCAGAGCCGGCAGAAAGACACAGACAGCAGGCGTTGTCAACAGACTAC	1059
Db	1060	CAACCCACACCCACAGAGGCGCGGACAGAAAGGCCACAGAGCCCGGTTATCACTGATAT	1119
OY	1060	GAGAAAGGTGAGGCTCTTTGGAAGACAGAGTTGGTGAAGCTGAGAGGCATCGTCAGAGAG	1119
Db	1120	GAGAAAGGTGAGGCTCTTTGGAAGAGAGCAAGTCAAGTGTGCTCCAGAGGACCTTGTGAAG	1179
OY	1120	AAGTGTCTCTCTTTGGCAAGAGAGTGTGATGAAGATGGAAGCCACACAGAA---	1176
Db	1180	AAACCTGCTCGGTTGGGACAGAAAGTGTGATGAAGAAATAGAGTCCACAGAGAGAG	1239
OY	1177	GTTGTTCAAGAGTCCACGTAACCTGTGGAGAACAGAGAGGACGAGGAGAGAGA	1236
Db	1240	GTTTGGCCCGAAGTCCAGTCAACACCTGTGGAGAGAGAAACGGAAGAGAGAAAC---	1295
OY	1237	GGAGAGGCTGAAGGGGGCGTGGTGAAGAAAGAAACAGAGAAATCTCTTGCCCTGAGAA	1286
Db	1296	-----GAGAGTGGAGAAAGAAACGAGGGGTCTGTGCGACCTGGAATA	1335
OY	1297	CTGCTGAGCCCGACAGAGGTCCCCCAGAGAAAGCTGAGACCTGTGAGAGACTGATGAAGC	1356
Db	1336	TGTGTTGGAAATGATGCAAGAACTCAGAGAAAGCCGAACCTGCCAAGAGACTGTTGAAGTC	1395
OY	1357	AGAGAGATGTGTCTCTGTGGAGAGACCAACTCAACTGACAGACCTTAAGTCTTGAAG	1416
Db	1396	AAAAGAAAGTGTGTTTCCGAGAGAGACCTTACACAGAGGAGTGCACCTCAAGTCTTGAAG	1455
OY	1417	AAGAGCGTGGCCAAACCCAGAAAGCAATTTGTCAGTGAAGTGGAGATGCTGTCTCTAG	1476
Db	1456	AAGTGTGTGTCCAAACCCCGAAGGCGTTGTGATGAAGTGGAAATCTGTCAACACAG	1515
OY	1477	GAAAGAAATCAAGGTACAGGGAATGCTTGAAGAAATCTTTGATAGTCAAGCGCTTAAG	1536
Db	1516	GAGAGAAATGAAGGTGAGGAGGAATCCACTTAAGAAAGCTTTTACACAGACTGCTTAA	1575
OY	1537	AAGCTGTCTGGGAAAGAGAGAGAGGAGAAACGAGAGGTGGGGGAGAGCAAGAGGCTTGA	1596
Db	1576	AAGCTTCTGGAAGAAACGAAAGGAGAAAGAGGAG---GAGAGAGAGAGAAATCAAGG	1632
OY	1597	GAATACCAACATTCATCACACCGAAATCCCGACAGAGTGTGATGACACAGAGAGAGAGC	1656
Db	1633	GAGACACTCAAGTTCACAGCCGATTTCTCCGAGAGCAGACAGAGAGCAAAAGGCGCAGAGC	1692
OY	1657	TCTGCTGTCGTCGCGGAGAGGAGGCTGAGAGAGACAGTGTCTGGAGAAAGGGGCGGTGGA	1716
Db	1693	TCTGCTCATATCCCTTGAGAGAGCCCGAGAGAGATACGTGTCTTGGAAAGGGGCTTGA	1752
OY	1717	GCACCCACAGATGGGGAAGCTGAAGAAAGAACTACTTCCGATGGAGAGAGAGAGAGAA	1776

Db	1753	GTGCAGCAGCGATGGGGAAAGCTGGAAGAAAGGAGCTACTTCCGATGTGAGAGAGAAAAAGAA	1812
QY	1777	GGGATCACTCCCTGGGATCCCTTCAAAAATATGTGTACACCCAGAAAGGGTCCGAAGA	1836
Db	1813	GGTGTCACTCCCTGGGATCAATTCAAAAAGATGTGTACCCCAAGAGAGCTGTGTAGACGG	1872
QY	1837	CCCTTCTGAGAGTGCAGAGGAGAAAGAGCTGTGAGAGGTCAGAGGCCACCTTGTCTCC	1896
Db	1873	CCTTTGGAAAGTGTATAAAGAAAGATGAGCTGTGACAGAGCTCAGAGGCGCTTACCTTGTCC	1932
QY	1897	ACTGATACACAGTGTCAAAATGCAAGATGAAGTCAAAACTGTGTGAGGACAACAAAG	1956
Db	1933	ACCGAGACACAGCTCTGAAATATGCAAGAAATMAAGGAGAGGTGGAAGGCCAAAG	1992
QY	1957	CCAGGGAACCAAGCGGTAGGGGTGAGTACTTCCAGTCTGTGGGAAGCACTGATTTGTCTC	2016
Db	1993	CCGGAGAACCAAAAGCCCAAGGTGATACCTCAGTACTTTGGAAAGCTTTAAATTTGTGTG	2052
QY	2017	GGATCATCCAGAAAGAGAGCAGAGAGGATCCTCTTCAGATGATGAAGAGGCGCCAAG	2076
Db	2053	GGATCATCCAGAAAGAGAGCAGAGAGGATCCTCTTCAGATGATGAAGAGGCGCCAAG	2112
QY	2077	ACACTGGAGGGGACAGTCAACAGCAGAGAGCCAGCAAAAGACAAAGAACCCGGAACA	2136
Db	2113	GCAATGGAGAGAGACACCAAGAAAGCTGATGAGCGCCGGAAGAACAGAGAGCGGGACA	2172
QY	2137	GACCGTGTCTCTGCACACCACCCAGAGCAGAGCCCAAGAGAAATCTCTCACCCGAG	2196
Db	2173	GACGGGATCTTGTGTGTCTCCCAAGAACATGATCCAGGGCAGGGAAGTCTCTCCCGGAG	2232
QY	2197	CCAGCGGGAAGCCCTTCCAGAGGGGAAAGGTGTCTCCACTTGGGAGTCAATTTAAAGATTA	2256
Db	2233	CAAGTGTGAACCTTACCAGAAAGGAGGGGCTTCCACCTGGGAGCTTTAAAGGTTA	2292
QY	2257	GTCACCTCCAGAAAAATCCAAAGTCAAACTGGAAGAAAAAGCCGAAGAC-----	2307
Db	2293	GTCAAGCCCAAAAAAATCAAAAGTCCAAAGCTGGAAGAAAAAGGAAAGACTTCATAGCT	2352
QY	2308	---TCTAGTGAAGAGAGTGTGTCCACTGAGATGTGAACCCAGTAGAGAAAGAACTTTGGGTT	2354
Db	2353	GGGTGTGTGTGAAGCAATTCCTCACTCCAGACACTGAAGCCCGTGAAGAAAGAAATCTGGGTT	2412
QY	2365	TCCATTAGAATTCATCCCCGAGCGGCGAGAAAAAGGGCAGAGCGGAGAGCAAGAACAA	2434
Db	2413	TCATCAAGAAGTTATTCTCGGACGAAGSAAAGAAAAAGGCCAGATGTGGAAACAGAACAA	2472
QY	2425	GCCACTGTGAAGACTCAGGGCCAGTGGAGATMAATGAGAGCAGACCTTAATGTCCAGCC	2484
Db	2473	GCCCTGTGTAAGACGCGAGGGCCAAACAGGGGCCCAAGCAAGATGACTGTATGTCCCGCC	2532
QY	2485	GTCGTCCTCTGTGTGAGTATTAATGCAGTGTGAGAGGGGAAGAAATGG-----AAGCC	2535
Db	2533	GTGTCTCTGTGTGAGTATGATGTCTGTGAAGAAAGGGAAGAAATAGAGGACAGCAACACC	2592
QY	2536	CAGGGAAATACGAGCTGCCCGCAGCTGTGAGGGGCTGTATGACTGTGCGAGAGCTCAGT	2595
Db	2593	CAAAAAAGCCGAGAGCAGCCCGAGCAGAAAGCAGCCAGCTGAGAGTGTCCAAGAGCTCAGC	2652
QY	2596	AAGACTTGTGTCCACTGTGAGTGTGCGCAGTCAATTAATGATGGAGCAAGGCAAGTCCAGT	2655
Db	2653	GAGAGTCAAGTTCAATGATGATGAGCAGCAGCTGTGCTGACGGGAGCGGACAGTCACTTT	2712
QY	2656	GTCGAAGAGCGGTCTCTTGTGTGATATCCGCTTCCGTTAACGAACCTTTGACACACA	2715
Db	2713	ATTGAAGAAAGTCTCTCTTGTGAATATGTCTTCAAGTACAGAAACCTTTGACAAAGTA	2772
QY	2716	GCGGGAAGAGCATGCCACCTGTTGAAGAGAGTCACTGAAAGAAAGACATCAATGG---AGAA	2772
Db	2773	GAACTGAAGCCGACTGTTAACTGTGAGAGAGTATTGGAAGAGAAAGTAAATGTCCAGAAAGAA	2832
QY	2773	GAAACTCTGTGTCAACCCAGAGCTTACAGAGAGGTAAAGATGCCCATAGCAGACATGTCT	2832

Dh 1884 TCTGCTTACCTCCCTGAGAGCCGAGAGATCACGTCTCTGGAAGAGGCTTAGCCGAG 1943
Oy 1717 GCACCCAGATGGGAGAGCTGAGAGAACTACTCTCGATGAGAGAAAGAGAGAA 1776
Dh 1944 GTGCGAGAGATGGGAGGATCAAGAGAGAGTACTTCCGATGGAGAGAGAAAGAGAA 2003
Oy 1777 GGGATCACTCCCTGGGCACTCTCAAAAAGATGTGACACCCAGAAACGGGTCCGAGAA 1836
Dh 2004 GGTGACTCCCTGGGCACTCAAAAAGATGTGACGCCCAAGGCGTGTGTAGACGG 2063
Oy 1837 CCTTGTAGAGTCAAGAGAGAGAGAGTGGAGAGTCAAGAGGCGCACTTGTGCTCC 1896
Dh 2064 CTTTGGAGAGATGAATGAAGATGAGTGGACAGGTCAAGGCGTACCTTGTCTTCC 2123
Oy 1897 ACTGATACAGAGTGTCAAGATGAAGTCAAAACTGTTGTGTGAGAGAGAAAG 1956
Dh 2124 ACCGAGAGCAGCGCTGTGAATGCAAGAAATGAAGAGAGGTGGAAGAGCCAAAG 2183
Oy 1957 CCAGAGAAACCAAGCGTGAAGTATCTTCAGTCTTGGGAAACACTGATTTGTCTC 2016
Dh 2184 CCGAGAAACCAAGCGGATACCTCAGTATCTTGGGAACTTAAATTTGTGTG 2243
Oy 2017 GGATATCCAAAGAGAGCAAGAGAGCATCTCTTCAAGATGAAGAGAGGCGCAAG 2076
Dh 2244 GGATATCCAAAGAGAGCAAGAGAGCATCTCTTCAAGATGAAGAGAGGCGCAAG 2303
Oy 2077 ACATGGAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2136
Dh 2304 GGAATGGAG 2363
Oy 2137 GACGCTGTTCTGCGCAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2196
Dh 2364 GACGGGATCTCTGCTGTGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2423
Oy 2197 CCAGGGGAG 2256
Dh 2424 CAAGGCTGGAAG 2483
Oy 2257 GTCACTCCAAAG 2307
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Oy 2365 TCCATTAAG 2424
Dh 2604 TCAATCAAG 2663
Oy 2425 GCCACTGTGAG 2484
Dh 2664 GCCCGTGTGAAG 2723
Oy 2485 GTCTGCTCTGTCTGTAGATTAATGCAAGAGAGAGAGAGAGAGAGAGAGAG 2535
Dh 2724 GTGTGCTCTGTCTGTAGATTAATGCAAGAGAGAGAGAGAGAGAGAGAGAG 2783
Oy 2536 CAGGGGAATAG 2595
Dh 2784 CAAAAAG 2843
Oy 2596 AAGACTGTGAG 2655
Dh 2844 GAGAGTCAAGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2903
Oy 2656 GTGGAAG 2715
Dh 2904 ATTTGAAG 2963
Oy 2716 GCGGGAAG 2772
Dh 2964 GAAGGTGAAG 3023

Oy 2773 GAACTCTGTGCTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2832
Dh 3024 GAACCCCCAG 3083
Oy 2833 ACCAGTGAAGTGAATTTACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2892
Dh 3084 GTTATGAGGCGGAATTTACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3143
Oy 2893 CGTACTGAAG 2952
Dh 3144 GGTTCGAAG 3203
Oy 2953 GTTTCAGAGTACTGACTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3012
Dh 3204 GTCTCCAGGTAAACGAGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3263
Oy 3013 GAGAGTGTGCTGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3072
Dh 3264 GAGGTGGCGTACTGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3323
Oy 3073 GTTGCAG 3129
Dh 3324 GTGCGAG 3383
Oy 3130 ACGGGTCAAG 3189
Dh 3384 CTTCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3443
Oy 3190 TCGGAG 3249
Dh 3444 CTGAAG 3503
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Oy 3307 GTACGCGAG 3341
Dh 3564 GTACAG 3623
Oy 3342 ---GGTATCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3399
Dh 3624 GGGGTAAATTCAG 3683
Oy 3400 TTGACAG 3459
Dh 3684 CTTACAG 3743
Oy 3460 ACACAG 3519
Dh 3744 ACCCAG 3803
Oy 3520 TCAACAG 3579
Dh 3804 TCAAGGAG 3863
Oy 3580 AATATGTTCCAG 3639
Dh 3864 AGTTTTGTGTCCAG 3923
Oy 3640 ACACAG 3699
Dh 3924 ACAGATAAAG 3983
Oy 3700 GAGGAG 3750
Dh 3984 GAGGCTGAG 4043
Oy 3751 GTGTTGTACACTCTGG-----ACCAACAGTCAAGAGAGAGAGAGAGAGAG 3804
Dh 4044 GGGTCTATGAG 4103

OY	3805	AGTGAAGGATGGGAGTGGCGGGGTCTCGAGAAAGAGAGATGACGAGTGCAGAG-----	3860
Db	4104	GGTGAAGGGACAGAGAAAGCTGTAATTAAGAAAGATGATGCTTGAAGTGCAGAGTAC	4163
OY	3861	-----TCCTTACCCTGGAGAGGAGAGATGGAAGTGAAGTGAAGGAGAGAA	3909
Db	4164	GCTAAGTCTCTCATTCATCCCGGTGGAGAGAGAGATGTGTAGTTCGAAGTGCAGAGAA	4223
OY	3910	AGGAGACCAAAAGCCAGAGCAAGTGAAGTGAAG--AAGGTGACGAGAGAAACAGCCGCTCT	3966
Db	4224	ACAGAAACCAAGCCAAACCCATGTGAATGAAGAGAAACCTTGACACAGAAACAGCTGTAC	4283
OY	3967	GAGCATGAGAGCACTTCAGGGAGCCAGTCTTGACACTTGACATGCCAGCTCAGAGAG	4026
Db	4284	GATATCTGAAGAGTCACTAAGACAGCTCTCCAGACAGTAAAGTGAATGATAGATGG	4343
OY	4027	GGGAGGACACTGGGGAACCTTGGAGGAGAGCCCTTC--TCCGACCAAGACCAACCA	4083
Db	4344	GCAAGAGAGTCAAGCACTTTGGAGAGAGAGCCCTCCTCGCTTGAAGTCAAGAGAGGAG	4403
OY	4084	GTTTGCATAGAGTTTCAAGTTTCAAAAGCTTGACACAAACAGTCACTCAAAACAGCAGAACT	4143
Db	4404	GTAATGACCAAAATATCAAGTTTCAAGTCTGAGGCAATGTTACCTTAACAGCGGCTGCA	4453
OY	4144	GTGCAAAAGTCAAT-----AGAACGTTTGTGATTTTCAGAGACAGGTGAAGTCCAGAG	4197
Db	4464	GAGAGAGAAAGGCTTGAAGAGAACTGCCCAATTTTGAAGAACAGGTGAAGCGTTGGAG	4523
OY	4198	TGTGTAGTGCACACTTATTACAGCTGAGAAAGTCTCTGCAAGCGGAGGCCACTGAGACT	4257
Db	4544	CTTCAGAGTGCACCTTTAGTTCTGGAAGAGAAATCTCTGAAAAAATTAAGACTTTGCC	4583
OY	4258	CTTCAGCATCAGAGAGCAAGGATGCCCTGGGGCCTGAGTCTCAGGACAGAAATCCATCCA	4317
Db	4584	GCTCATCAGAGGGAAGATGCTGTGCCACAGGGCCCGAGTGTCAAGCAAAATTCAGACACA	4643
OY	4318	ATCATTAATACTCTGCTCTGAAAGCACACCCTTACATCTGACCTTCAAGAGAAATAAGC	4377
Db	4644	GTGTATGATATCTGCTTACTACCAAGAAAGGCTTAAGTTCGACCTGGAAGAGAGAAACC	4703
OY	4378	GCAATCCAGAGAGAGCATCAGAGAGAGAAAGCAAGCCAGATGCTGGATCGATAGCTGAC	4437
Db	4704	ACATCATCTGAAGTGAAGTCAATGTAAGTGCATGACAGAGTTGCTTGCC-----AGAG	4757
OY	4438	GGCAAGAGAGTACAGCAATCGAAAAAGTCTCAAGGCTGGAAGCTGAGATCCTGGAATT	4497
Db	4758	GTCAAATGAGTGTGAAGAAATG---AGATTTAAGAGCCCTGAAAAATGGGATTTTGGAACTT	4814
OY	4498	GAGAGTAAAGCAACAGATTGTGCTGAAGCTGATTCAGACAGCCGTTGACCACTTGCCA	4557
Db	4815	GAGACCAAAAGCAGTAAATCTTGTCCAAAACATATCCAGACAGCCGTTGACCAAGTTSTA	4874
OY	4558	CGTAC--ACAAAACAGCCCCGAAACTCATGCTTATGATTCACACACCAGATTCCTGCA	4614
Db	4875	CGTACAGAAACAGACAGCCAGAAATGTTGACGCTGTGAGTTACAGACACAAAGCTTCAG	4934
OY	4615	TGCAGGCTTGACAGACAGCA	4634
Db	4935	ATAAAGCTGACAGCCAGGA	4954
RESULT 5			
US-09-880-107-3439			
: Sequence 3439, Application us/09880107			
: Patent No. US20020142981A1			
: GENERAL INFORMATION:			
: APPLICANT: Horne, Darci T.			
: APPLICANT: Vockley, Joseph G.			
: APPLICANT: Scherf, Uwe			
: APPLICANT: Gene Logic, Inc.			
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
: FILE REFERENCE: 44921-5028-WO			
: CURRENT APPLICATION NUMBER: US/09/880.107			

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: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: Patencin Ver. 2.1
: SEQ ID NO 3439
: LENGTH: 6608
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 U81607
US-09-880-107-3439

Query Match      37.4% Score 1945.6; DB 10; Length 6608;
Best Local Similarity 67.5%; Pred. No. 0; Mismatches 1324; Indels 243; Gaps
Matches 3253; Conservative 0;

QY 1 ATGGGCGCAGGAGTGTCCACCGAGCAGCGAGCCCGGACACCGCG---GGGAGCGAC 57
Db 192 ATGGGCGCGGGAGGCTCCACGAGCAGCGACCGGAGCAGCCCGGAGAGGAGCTCC 251
QY 58 ACCCGAGCGAGCTGTGTCTAGTGTGGCCATGGGCGCGGACGTGAAGCCTCGGGA----- 111
Db 252 ACCCGCGGTGACCCCGAGCCGAGCGGCGGCGCCCTCGGCGGAGGCGGCGCAGACACC 311
QY 112 ---GGAGCTGGAGACCCCGCGAGCCCGGACCCCGGACCAACTCCCAACAGAAATGGC 168
Db 312 ACCCGGAGACCCCGCGCATGCTCTCTGGAGCCCGCGCACCAACTCTCTAAGAAATGGT 371
QY 169 CAGCTGTCTTCTGTCAACGGCGTACTGTGAACAGAGATGTCTATGTCCAAAGAGAAAC 228
Db 372 CAGCTGTCCACCATCAATGATGGCGTACTGTAGCAAGATGAGCTTCAGAGAGGTGAC 431
QY 229 CAGGAGG-----GCAGAGGAA 246
Db 432 CTAAATGGCCAGAAAGAGGCCCTGAAAGGTCAAGAGCCCTAAACAGCCAGAGAGAA 491
QY 247 GAAAGTCGTTGATGAGATGTTGGACAGGAGGAGTGCAGAAATGTGAGAAAAAGACCA 306
Db 492 GAAAGTCATTTGTACGGAGGTGGACAGAGACTGTGAAGATGTAGCCAAAGAGACTCC 551
QY 307 GTTGAAGAAATGGCGGCACTCCACAGCTGTTGAAGATATACAAAGATGGCGAGAG 366
Db 552 GATTAAGATAGGTGCTACTAGTACAGCGGTGTTCACGACATACAGATGATGGCAGGAG 611
QY 367 GAGACATCAGAAATATTGAACAGATCCCTGCTTCAGAAAAACAATGTGGAAGAAATGTA 426
Db 612 GAGA---ACCGAAATATCGAACAGATCTCTTCTCAGAAAGCAATTTGAAGAGTACA 668
QY 427 CAGCGTCTGATCCCGAGGCTAATATGTTGGCTTCAGAAAGTATTTAATTTTGTGT 486
Db 669 CAACCCACTGATGCCAGGCTAATATATATTTGAATTAAGAGGTATTAAGTTTGTGGC 728
QY 487 TTTAATTCACGCGTAAGAGATTAATAATGAAGTACAGTACTGTCCAACTACTACT 546
Db 729 TTTAATTCACGCTGTAAGAAAGATTAAGACAGAAAGCTGTACACTGTCCAGTACTACT 788
QY 547 GTCAAGAAAGATGAAGGCGAAGGGCAGAAAGCCCTGTGTGGAAGTGGAGACCCAGAGAG 606
Db 789 GTGAAGAAAGATGAAGGGAGGAGGAGCAGAGA-----GGGCGTGGGAGCACCAAGAG 839
QY 607 CCCAGTGTGGAAGCTGCGGTGCGAAGTGCAGATCCAAAGAAAGTGAAGTGAAGCAATCC 666
Db 840 CCCAGCTTGGGGCT-----GGAAGACAGATCCAAAGAAAGCAACCCAAACACT 893
QY 667 ACAGAGAAAGAAAGGAGCCCTGAAGCAAGAACAGAGACAGACAGAAATCCCTCTCA 726
Db 894 ACAGAGAAACCCGAAAGAACCTTGAAGGTGTGAGCAAGAGCCAGCAGAAATTTCTCCCA 953
QY 727 GCCGATCTGTATCAAGCGGCTGAGGAAAGCAAGATGAAGGAGAAAGAAACAGAG 786

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[illegible]

OY	1837	CCCTCTGAGAGTGCACAGAGAGAGAGAGCTGAGAGAGTGCACAGAGCCACTTGCTGCC	1896
OY	1837	CCCTCTGAGAGTGCACAGAGAGAGAGAGCTGAGAGAGTGCACAGAGCCACTTGCTGCC	1896
Db	2064	CTTCTGGAAAGTGTATTAAGAAATGAGCTTGAGACAGAGCTCAAGAGCGCTTGTGCTTCC	2123
OY	1897	ACTATATGACACAGTGTACAGAAATGCACAAAGATGAAAGTCAAAACCTGTTGTGAGAACAAAG	1956
Db	2124	ACGAGAGACAGAGCTGTGAATATGCAAAGAAATGAAGAGGAGCGTGGAAGAGCCAAAG	2183
OY	1957	CCAGAGAGACCAAAAGCTAGGGTGGATACTTCAAGTGTCTTGGGAAGCACTATTTGTGTG	2016
Db	2184	CCGGAAGAACCCAAAGGCCAAGGGTGGATACCTCAATCTTGGGAAGCTTTAATTTGTGTG	2243
OY	2017	GGATCATCCAAAGAGAGAGAGCAAGAGGCACTCTTTCAGATGATGAAGAGAGGCCCAAG	2076
Db	2244	GGATCATCCAAAGAAAGAGAGCAAGAGAGTCTCTTCTGATGAGGAAGGGGGAGCCAAAA	2303
OY	2077	ACACTGGAGGGGACAGTGCACAGAGAGAGAGGCCAGCAAAAGACAAAGAGCCGGAAACA	2136
Db	2304	GCAATGGGAGAGACACCACCAAGAAAGCTGATGAGGGCCGAAAAAGACAAAGAGAGCCGGGACA	2263
OY	2137	GAGCTGTCTCTGCAACACCCAGAGAGAGAGACCAAGGSCAAAGGCAAGAAATTCCTCACCCGAG	2166
Db	2364	GAGCGGATCCTTGCTGTGTTCCCAAGAACATGATCCAGGGCAGAGGAATTCCTCCCCGGAG	2423
OY	2197	CCAGCGGGAGAGCCCTTCCGAAGGGGAAAGTGTCTCCACTTGGAGATCATTTAAAAGATTA	2256
Db	2424	CAAGCTGGAAACCTTACCGAAAGGGAGGGGCTTTCACCTGGGAGATCATTTAAAAGGTTA	2483
OY	2257	GTCACATCCAGAAAAAAATCCAACTCAAAACGTGGAAAGAAAGAGCCGAGAC-----	2307
Db	2484	GTCACGCCCAAAAAAAATCAAAAGTCCAAAGCTGGAAGAGAAAGGAGAGACTCCATAGCT	2543
OY	2308	--TCTAGTGTAGAGCAGTGTGTCACCTGAGATGGAACCGAGTAGAGAAATCTGSGT	2364
Db	2544	GGGTCTGGTGTAGAACATTTCCACTCCAGACACTGAACCCGGTAAAGAAATCTGGGTG	2603
OY	2365	TCCATTAAAGAAATTCATCCCGGAGCGGAGAAAAAGGCCAGACGGAGCAGAGACAA	2424
Db	2604	TCAATCAAGAAATTTATTCCTGCGACGAGAGAAAGAAAGGCCAGATGTGGAAACAAACAA	2663
OY	2425	GCCACTGGGAAGACTCAGAGGCCACAGTGAAGATTAATGAGAGACGACCTTAATCTCCACGC	2484
Db	2664	GCCCTGTTGAAGACGAGAGGCCAACAGAGGCCAACAGAAAGATGACTCTGATGTCCCCGGCC	2723
OY	2485	GTCGTGCTCTGTGTGAGTAAATGCAAGTGAGAGGGAGGAAGATGG-----AACCC	2535
Db	2724	GTCGTGCTCTGTGTGAGTAAATGCAAGTGAGAGGGAGGAAGATGGAGGACAGCAAGCC	2783
OY	2536	CAGGGGAATACAGGAGCTGCCCCAGACTGTGTGGGGGCTGTGAAGTGTCCGAGGAGTCACT	2595
Db	2784	CAAAAAAGCGAGAGACAGCCCGAGCAAAAGCAGCCACTGAGGTGTCCAAAGAGCTCAAGC	2843
OY	2586	AAGACTGTGTCACACTGTGAGTGTGAGTGTGATTTGATGGAGACAGGGCACTATCCAGT	2655
Db	2844	GAGAGTCAAGTTCATATGATGAGGACAGCAAGCTGTGCTGACAGGGGACGAGGCACTCACTT	2903
OY	2656	GTCGAAGAGGCTCTCTCTTGCTGGATATCCGCTTCGCTAACAAGAACCTTTGACACACA	2715
Db	2904	ATTGTAAGAAAGTCTCTCTTGGAATATGCTTTCAGTACAGAAACCTTTGATACAAAGTA	2963
OY	2716	GCGGGAGAGGCAATGCCAAGCTGTGAAGAGGTGACAGAAAAAGACATCTATTCG---AAGA	2772
Db	2964	GAGCTGAAGCCGACACTGTTAAGTGAAGAGGTATTTGAAAGAGAAAGTAATTTCCAGAAAGAA	3023
OY	2773	GAAGACTCTGTGTCACCCAGAGCTTACAGAGAGTAAAGATGCCCATGACGACATGTGCT	2832
Db	3024	GAAACCCCAAGGTTACTGTGAACCTCTCCAGAGAACAGAGAGGCCCGGGGCGACAGGCTC	3083
OY	2833	ACCAAGTGAATGATTCACCTCAAGAGCTGTGTACAGCCACAGAGACCTCAAGAGCTCTC	2892
Db	3084	GTTATGTGAGGGGAAATTAAGCCCCGGAAGCTGTACAGCTGTACAGAAATCTCAGAGGCTATTG	3143

OY	2893	CGTACTGAAAGATTACCGAAGCATGGGGGGCCGAAGACACACAGACATGGGTGTCCCA	2952
Db	3144	GGTTCCGAGAGAGAACCCGAAGCATCTGCTGTGAAGAGAACACAGAAATGGTGTCCACA	3203
OY	2953	GTTTCCAGCTGATGATCTCCCCAGACACCACAGAGAGAACCCACCCAGTTCTAGGAGSTA	3012
Db	3204	GTTCTCCAGTTAAACCGACTCCCCAGACACACAGAGAGAGCCACTCTCGGTAGGAGAGTG	3263
OY	3013	GAGAGTGGTGTGCTAGTATACAGAGAAAGAGAGCCCGACAGCCAGGCCATCTCTCCAAACC	3072
Db	3264	GAAAGTGGCCGCTACTGTGCATATGAAAGAGCAAGAGAGCCGAGACTCAAGAGGTCTCTCAGSCA	3323
OY	3073	GTTCCAGCAAGGGGAAAGAGAGATCCCGAGTGCCTTCGAACC---CAACATGTGCAGAGA	3129
Db	3324	GTGGCAGAAAAAGTGAAGAGGAATCCAGCTCCGTGCAGCGGTGGGGCCAAAGATGTG	3383
OY	3130	ACGGGGCTCAAAAGCAGCTGAGAGAGTGTGAAGAGAGTATGAGAGAGAGCTCCCAATGTGTGCT	3189
Db	3384	CTTCAGGCTGTGCAGAGACAGAGCCAGAAAGACAGAAAGACAGAGCTTGAAGCTGTGGGT	3443
OY	3190	TCGAGAGAAAGAGAAAGACGTTATCCGAAAAGACCCGTCAGAGAACTGGAAGCTGAGCAT	3249
Db	3444	CTGAAGAAAGAGACGAGTATGATGTGTTGAAAGTATGATGTCTCAGAGAGCAAAAACTAGCGCT	3503
OY	3250	CTTGACACAGGCTCTGAGACTGGAACAGGCTACTCCAGAGAGCCTTG---AAGTCTCTAA	3306
Db	3504	TTTATACAAAGGGAAGGTGTGGGGGAGACCACCCAGAAAGGTTTGA AAAAGTCTTCAA	3563
OY	3307	GTCACGGCAGATGTA-----GACCAATGTCCAGCTGCCA-----	3341
Db	3564	GTCACAGAGACATATAGTGTCTAGTGAAGCTTTGTACCACTGTTCGAAGCCGAAACCTTAAGCT	3623
OY	3342	--GGTTATCAAGCTCCAGACGCTGATGGAACAGAGCCGTTGGCCCTGATCATCCGAAAC	3399
Db	3624	GGGGTAAATATCACAGAGAGATGTGATGGAACAGAGCTATCCCCCTGACGTGGTGA AAC	3683
OY	3400	TTTGACACAGTGAAGCAATATGGAAGCACTCCCTTAGCAGATTCAGACACTGCAGATGG	3429
Db	3684	CTTACACACAGTGAAGTATGGAAGCAACCCCGCTGTGCGAATTGAGACACACAGGACA	3743
OY	3460	ACACAGCAATGTAACCATTTGACACCCAGACAGTAAAGCCACTGCAGCTGCAGGAG	3519
Db	3744	ACCCAGAAAGACAGATTTGTGGAAATCCATGAGAGAAATGAGGTGCCATCTGTGTACCCAG	3803
OY	3520	TCACAGGTCAAGAGAGAGAGGGGCTACTGCTCAGAAAGAGAGAGCTTCGACACTACT	3579
Db	3804	TCAGGGGGCACAGAGAGAGGAGGAGTTCCTGCACAGAAAGAGAGGCTTCAGACACTCC	3863
OY	3580	AATATATGTTCCAGCCACAGAGAAACATATGGGGAAGAACAGAGAGATGTTCTTGAACCT	3639
Db	3864	AGTTTTTGTGTTCCAGGAAAGAACTAAAGAAACATCAAAATATGGAAGACACTCTAGAGCAT	3923
OY	3640	ACACAGCAAGAGCTTACTGCTGCAGGCGGCGCTTGTGGCAAAACATGAGGTGGGTCAA	3699
Db	3924	ACACATTAAGAGGTGTACGTGGAACCTGTATTCATTCTGTCAAAAGCTGAGGGGCTCAA	3993
OY	3700	GAGGGTGA-----GGTTGAACTGTTGTGATGAGAAAGAAAGTCAAAAGAGAACAGAG	3750
Db	3984	GAGGCTGACCAAGTATGCTGTATGAGAAACCAAGACGTACATTTTGTGAAGAGACTGTAG	4043
OY	3751	GTTGTTTATACACTCTG-----ACCCAACAGTCAAAAGGCTGTGATGTGACATATGAC	3804
Db	4044	GGGCTCTTAACACAGGCTATMACAGTCACTGCGGAAAGAGTCACTGAGAGTTGCCCTTAAA	4103
OY	3805	AGTAACTGATGGAGAGGCGCGGGGTCTCAGGAAAGAGAGTCAAGTCAAGTGCAGAG---	3860
Db	4104	GGTAAAGGACAGAGAAAGCTGTGATGTAAAAGAGATGATGCTTTGAACTGCAGAGTCA	4163
OY	3861	-----TCTTAAGCTCGAAGAGGAGAGATGGAAGCTGAGCTTGAAGAGAGAA	3909
Db	4164	GCTAAGTCTCTCTCATCTCCCGCGTGGAGAGAGAGATGTGTTCAGTGTGAAAGAGAGAA	4223
OY	3910	AGGAGACAAAGCCAGAGCAATGATGTGAAG---AAGGTGACAGAGAAACAGCCGCTCT	3966

Db	4224	ACAGACGACGAGCCACCCCTTGTGAATGAAGAGACCTTGGACACGAAACAGCTGTTACCC	4283
Oy	3967	GAGCATGAAGAACCTCAGGGAAAGCCAGTCTCGACACTTGGACATGCCAGCTCAGAGAG	4026
Db	4284	GTATCTGAAGAGGTCACTAAGACAGCTCTCCACACAGTGAATGTCCATCATATATATGG	4343
Oy	4027	GGGAAGGCACCTGGGAAGCCTTGGAGAGAGCCCTTCTC---TCCACAGCCACAGCAAGCA	4083
Db	4344	GCAAAAGGAAGTCACACACTTTTGGAAAGAGCCCTCTCCCTGAGCTTACAGAGAGCA	4403
Oy	4084	GTTTGCATAGAGGTTCAAGTTCAAGCCTGGACACAGAGTCACTCAAAAGCCAGAACCT	4143
Db	4404	GTATGACACCAAAATTCAAGTTCAAGTTCAGAGCTTGAAGCATCTTACCTTAAACGGGCTGCA	4463
Oy	4144	GTGGAAGAAGTCAT-----AGAAAGCGTTGTGATTTTCAGACAGAGTGAAGTTCACAG	4197
Db	4464	GAGAGAGAAAAGGTCTTAGAGAGAACTGCCACACTTTTGAAGAACAGTGAAGCGTTGGAG	4523
Oy	4198	TGTGTAGTGCACCTTATTATACAGCTGAGAAAGTCTCTGCAAGSGGTGGCCACTGGACT	4257
Db	4524	CCTCAGAGTGCACATTTAGTTAGTTCTGGAAGAAATCTCTGAAAAAATGAAGACTTTGCC	4583
Oy	4258	CTTAGCATGACAGAGACACAGGTATCCCTGGGGCTCGAGTCTCAGGCAAGATCCATGCCA	4317
Db	4584	GCTCATCCAGGGAAGATGCTGTGCCACAGGGCCGCACTGTACAGCAAAATCGACACCA	4643
Oy	4318	ATCATTTAGTAACCTCTGCTCTGAAAGCACCCCTCATCTGACTTCAAGAGGAATATAGC	4377
Db	4644	GTGATAGTATCTGCTACTACCAAGAAAAGCTTATAGTTCGACCTGGAAAGAGAGAAAAAC	4703
Oy	4378	GCATCCAGAGAGAGCAGTACAGAGAAAGAGACAGCCAGATGCTGTCTGATGCTGAC	4437
Db	4704	ACATCATCTGAAGTGAAGTCAAGATGAAGTCAAGTGAAGTGTCTTGGC-----AGAG	4757
Oy	4438	GGCAGAGAGGTACAGCAATCGAAAAAGTCTCAAGGCTGAACCTGAGATCCTGGAATTT	4497
Db	4758	GTCAAAGTGAAGTGAAGCAATTTG---AGGATTTTGAAGCCTGAAAAATGGGATTTTGGAACTT	4814
Oy	4498	GAGAGTAAAGCAACAGATTTGTGCTGAAGGTCATTCAGACAGCCGTTGACAGTTGCCA	4557
Db	4815	GAGACCAAAAGCAGTAACTTTGTCAAAACATCATCAGACAGCCGTTGACAGTGTGTA	4874
Oy	4558	CGTAC---AGAAACAGCCCCGAAACTCATGCTTATGATTTCAGAGCCAGGTTCTGGCA	4614
Db	4875	CGTACAGAGAAGACAGCCAGAAATGTTGAGCTGTGAATTACAGACACAAAGCTCAGTG	4934
Oy	4615	TGCAGGCTTGACAGCAGGCA 4634	
Db	4935	ATAAAGCTGCACAGCCAGGA 4954	
RESULT 6			
US-10-101-487-74			
: Sequence 74, Application US/10101487			
: Patent No. US20020169125A1			
: GENERAL INFORMATION:			
: APPLICANT: LEUNG, DAVID W.			
: APPLICANT: BERGMAN, PHILIP A.			
: APPLICANT: LOFOTIST, ALAN			
: APPLICANT: PIETZ, GREGORY E.			
: APPLICANT: TOMPKINS, CHRISTOPHER K.			
: APPLICANT: MAGGONER JR., DAVID W.			
: TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES			
: TITLE OF INVENTION: THERMOF			
: FILE REFERENCE: 07/319/0329			
: CURRENT APPLICATION NUMBER: US-10/101,487			
: PRIOR FILING DATE: 2002-03-20			
: PRIOR FILING DATE: 60/277,705			
: NUMBER OF SEQ ID NOS: 116			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 74			


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RESULT 8
US-10-101-487-71
; Sequence 71, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGSONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(522)
US-10-101-487-71
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Query Match          1.7%: Score 89.6; DB 9; Length 522;
Best Local Similarity 50.2%; Pred No. 2.6e-13;
Matches 221: Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY  905 AGAATCAAAAGAGATGATCTGAAACTGCCGAGAGAAGAAAGCAAGCAGAGAAA 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  5  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAAAGAAAGAGAAAGAAAG 64

QY  965 AAGTGCAGCAGAGAGAAAAGAAAAGACAGACAGCCCTCGAGAGACAGAGCCGCGCAG 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  65  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 124

QY  1025 AAGACACAGACCAGGCCAGGTGTGCAGAGACTAGCAGAGAGTGGAGCTCTTTGGAG 1084
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  125  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAAAGAGAGAGAAAGAAAG 184

QY  1085 ACCAGGTTGTGACCTGAGAGCATGTCAGAGAGAGAGTGTCTCTTTGGCAGCGAAG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  185  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 244

QY  1145 TGTTTGATGAGAAAGATGGAAGCCCAACAAGAAATTGTCAGAGTCCACGTGACACCG 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  245  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAAAGAGAGAAAGAGAGAAAGAAAG 304

QY  1205 TGGAAACAGACAGAGAGAGAGCAGAGAGAGAGAGAGAGCTTAAGGGCGCTGTGTG 1264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  305  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAGAGAAAGAGAGAGAGAAAGAAAG 364

QY  1265 AAGGAACAGAGAAATCTTGGCCCCCTGAGAAATCTGCTGAGCCCGAGAGTCCCCCAGG 1324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  365  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAGAGAAAGAGAGAGAGAAAGAAAG 424

QY  1325 AAGCTGAGCCTGTGAGAG 1344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  425  AGGAAGAGGAAGAAAGAGAG 444
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RESULT 9
US-10-101-487-73/c
; Sequence 73, Application US/10101487
; Patent No. US20020169125A1
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; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGSONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(530)
US-10-101-487-73
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Query Match          1.7%: Score 89.6; DB 9; Length 530;
Best Local Similarity 50.2%; Pred No. 2.6e-13;
Matches 221: Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY  905 AGAATCAAAAGAGATGATCTGAAACTGCCGAGAGAAGAAAGCAAGCAGAGAAA 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  526  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAAAGAAAG 467

QY  965 AAGTGCAGCAGAGAGAAAAGAAAAGACAGACAGCCCTCGAGAGACAGAGCCGCGCAG 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  466  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 407

QY  1025 AAGACACAGACCAGGCCAGGTGTGCAGAGACTAGCAGAGAGTGGAGCTCTTTGGAG 1084
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  406  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 347

QY  1085 ACCAGGTTGTGACCTGAGAGCATGTCAGAGAGAGAGTGTCTCTTTGGCAGCGAAG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  346  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 287

QY  1145 TGTTTGATGAGAAAGATGGAAGCCCAACAAGAAATTGTCAGAGTCCACGTGACACCG 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  286  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 227

QY  1205 TGGAAACAGACAGAGAGAGAGCAGAGAGAGAGAGAGAGCTTAAGGGCGCTGTGTG 1264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  226  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 167

QY  1265 AAGGAACAGAGAAATCTTGGCCCCCTGAGAAATCTGCTGAGCCCGAGAGTCCCCCAGG 1324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  166  AGGAAGAGGAAGAAAGAGAGGAAGAAAGAAAGAGAGAGAAAGAGAGAAAGAAAG 107

QY  1325 AAGCTGAGCCTGTGAGAG 1344
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DB  106  AGGAAGAGGAAGAAAGAGAG 87
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RESULT 10
US-10-101-487-69
; Sequence 69, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGSONER JR., DAVID W.
```

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; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 69
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
; US-10-101-487-69

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Query Match          1.7%; Score 89.6; DB 9; Length 554;
Best Local Similarity 50.2%; Pred. No. 2.7e-13;
Matches 221; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

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QY 905 AGAATCAAAAGAGATGATCTGAAACTGCCGAGAGAAGAAAGAGCAAGAGCGAGAAA 964
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DB 17 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAAAGAGAAAGAAAG 76

QY 965 AAGTAGACGAGGAAGAAAAGAAAAGACAGACCAGCTCGAGAGAGCAGAGCCGGCAG 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAAAGAGAAAGAAAG 136

QY 1025 AAGACACAGACCAGGCCAGCTGTGACGACTACGAGAGAAGGTGAGAGCTCTTGGAG 1084
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 AGGAAGAGGAAGAAGAGAGGAAGAAAGAGAGAAAGAGAAAGAGAGAAAGAAAG 196

QY 1085 ACCAGGTGTGACCTGGAGGCATCGTCAGAGAGAAAGTGTCTCTTGGCAGCGAAG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 197 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAAAGAGAGAAAGAGAAAGAAAG 256

QY 1145 TGTTCATGAGAGATGGAAGCCCAACCAAGATTGTTCCAGAGTCCAGCGAGACCG 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 257 AGGAAGAGGAAGAAGAGAGGAAGAAAGAGAGAAAGAGAGAAAGAGAGAAAGAAAG 316

QY 1205 TCGAGACAGCAGAGAGAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 317 AGGAAGAGGAAGAAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 376

QY 1265 AAGGAACAGGAGAAATCTTGGCCCTGAGAAACTGGCTGAGCCCGAGAGTCCCCCAG 1324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 377 AGGAAGAGGAAGAAGAGAGAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 436

QY 1325 AAGCTGAGCCTGCTGAGAG 1344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 437 AGGAAGAGGAAGAAGAGAGAG 456

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RESULT 11
; US-10-101-487-106
; Sequence 106, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: BERGMAN, DAVID W.
; APPLICANT: LEUNG, DAVID A.
; APPLICANT: LOROUIS, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMKINS, CHRISTOPHER K.
; APPLICANT: WAGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487

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; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 106
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(537)
; US-10-101-487-106

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Query Match          1.7%; Score 89.6; DB 9; Length 554;
Best Local Similarity 50.2%; Pred. No. 2.7e-13;
Matches 221; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

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QY 905 AGAATCAAAAGAGATGATCTGAAACTGCCGAGAGAAGAAAGAGCAAGAGCGAGAAA 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAGAGAGAGAAAGAG 76

QY 965 AAGTAGACGAGGAAGAAAAGAAAAGACAGACCAGCTCGAGAGAGCAGAGCCGGCAG 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAAAGAGAGAAAGAG 136

QY 1025 AAGACACAGACCAGGCCAGCTGTGACGACTACGAGAGAAGGTGAGAGCTCTTGGAG 1084
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAAAGAGAGAAAGAG 196

QY 1085 ACCAGGTGTGACCTGGAGGCATCGTCAGAGAGAAGTGTCTCTTGGCAAGGAAG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 197 AGGAAGAGGAAGAAGAGAGGAAGAAAGAGAGAAAGAGAGAAAGAGAGAGAGAGAGAG 256

QY 1145 TGTTCATGAGAGATGGAAGCCCAACCAAGATTGTTGCAAGTCCACGTAGCACCG 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 257 AGGAAGAGGAAGAAGAGAGGAAGAAAGAAAGAGAGAAAGAGAGAGAGAGAGAAAGAG 316

QY 1205 TCGAGACAGCAGAGAGAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 317 AGGAAGAGGAAGAAGAGAGGAAGAAAGAGAGAGAAAGAGAGAGAGAGAGAGAGAAAG 376

QY 1265 AAGGAACAGGAGAAATCTTGGCCCTGAGAAACTGGCTGAGCCCGAGAGAGTCCCCCAG 1324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 377 AGGAAGAGGAAGAAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 436

QY 1325 AAGCTGAGCCTGCTGAGAG 1344
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DB 437 AGGAAGAGGAAGAAGAGAGAG 456

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RESULT 12
; US-09-864-761-20733
; Sequence 20733, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 20733
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005822.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
; OTHER INFORMATION: NT HIT: AFI85255.1, EVALUATE 4.80e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE071749.1, EVALUATE 5.80e+00
US-09-864-761-20733
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Query Match 1.4%; Score 71; DB 10; Length 575;
Best Local Similarity 53.3%; Pred. No. 1.7e-08;
Matches 172; Conservative 0; Mismatches 150; Indels 1; Gaps 1;
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QY 937 GGAAGAGAAAGAGACAGCAGAAAAGTAGACGAGGAA-GAAAGGAAAAGACAGA 995
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DB 212 GAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 996 GCCAGCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1055
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 GGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 331
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1056 CTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 1115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 332 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1116 GGAAGAAGTCTCTCTTTGGCAACGGAATGTTTATGTAAGAGATGGAAGCCACCAAGA 1175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 392 GGAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

QY 1176 AGTTGTTGCAGAGTCTCCAGTCGAGCACCCTGGAGAAAGAGAGAGAGAGAGAG 1235
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 452 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1236 AGCAGAGCTGAAGGGGGCGCTGG 1258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 512 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 534
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RESULT 13
US-09-864-761-3972
; Sequence 3972, Application us/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 3972
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005822.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
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OM protein - protein search, using sw model

Run on: December 9, 2002, 21:27:58 ; Search time 39 Seconds
(without alignments)
1204.077 Million cell updates/sec

Title: US-08-978-277A-4

Perfect score: 8073
Sequence: 1 MGAGSTFQSRPEQFAGSDT.....AMAPRKCLPRLQLKAPYSK 1596

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5421.5	67.2	1346	2	US-08-635-121-2
2	4274.5	52.9	1780	1	US-08-769-309A-5
3	4274.5	52.9	1780	1	US-08-994-570-5
4	952.5	11.8	292	1	US-08-769-309A-3
5	952.5	11.8	292	3	US-08-994-570-3
6	656	8.1	651	1	US-08-769-309A-17
7	656	8.1	651	3	US-08-994-570-17
8	639.5	7.9	453	1	US-08-769-309A-14
9	639.5	7.9	453	3	US-08-994-570-14
10	521.5	6.5	396	1	US-08-769-309A-15
11	521.5	6.5	396	3	US-08-994-570-15
12	462	5.7	1786	4	US-08-973-462-8
13	388	4.8	1805	1	US-07-853-913-2
14	365.5	4.5	3696	4	US-09-134-001C-5080
15	361.5	4.5	2101	1	US-08-466-380-4
16	361.5	4.5	2101	1	US-08-470-950-4
17	361.5	4.5	2101	1	US-08-467-781-4
18	361.5	4.5	2101	2	US-08-483-924-4
19	361.5	4.5	2101	4	US-09-452-294-1
20	361	4.5	2137	4	US-09-134-001C-4463
21	358.5	4.4	2101	1	US-08-195-487-4
22	358.5	4.4	2101	5	PCT-US93-06160-4
23	354	4.4	1618	1	US-07-853-913-4
24	354	4.4	2409	6	5180808-2
25	334.5	4.1	1162	2	US-08-728-323A-2
26	334.5	4.1	1162	2	US-09-298-568-2
27	334	4.1	1018	1	US-08-072-610-2

28	334	4.1	1018	2	US-08-719-822B-2	Sequence 2, Appl1
29	334	4.1	1018	4	US-09-092-458-2	Sequence 2, Appl1
30	321	4.0	1852	1	US-08-425-061-24	Sequence 24, Appl1
31	321	4.0	1852	2	US-08-825-886-24	Sequence 24, Appl1
32	321	4.0	1863	1	US-08-425-061-16	Sequence 16, Appl1
33	321	4.0	1863	1	US-08-480-784-2	Sequence 2, Appl1
34	321	4.0	1863	1	US-08-483-553-2	Sequence 2, Appl1
35	321	4.0	1863	1	US-08-487-002-2	Sequence 2, Appl1
36	321	4.0	1863	1	US-08-483-554B-2	Sequence 2, Appl1
37	321	4.0	1863	1	US-08-488-011B-2	Sequence 2, Appl1
38	321	4.0	1863	2	US-08-825-886-16	Sequence 16, Appl1
39	321	4.0	1863	4	US-08-850-727-2	Sequence 2, Appl1
40	321	4.0	1863	5	PCT-US95-10202-2	Sequence 2, Appl1
41	321	4.0	1863	5	PCT-US95-10203-2	Sequence 2, Appl1
42	321	4.0	1863	5	PCT-US95-10220-2	Sequence 2, Appl1
43	320	4.0	1898	1	US-08-056-200-94	Sequence 94, Appl1
44	320	4.0	1898	4	US-08-800-644-94	Sequence 94, Appl1
45	319.5	4.0	1939	4	US-09-310-187A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-635-121-2
Sequence 2, Application US/08635121
Patent No. 5910442
GENERAL INFORMATION:
APPLICANT: Gelman, Irwin H.
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,121
FILING DATE: 19 APRIL 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: A30558 - 165/33603
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1346 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-635-121-2
Query Match 67.2%; Score 5421.5; DB 2; Length 1346;
Best Local Similarity 91.6%; Pred. No. 0;

Matches 1098; Conservative 24; Mismatches 62; Indels 15; Gaps 7;

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Qy 387 MEAHOEVAEVAEVSIVTEKTEEEEOGGGGEAGGVVETGTESEI:PPKEKLAPEOPEOBAEA 446
Db 1 MEAHOEVAEVAEVSIVTEKTEEEEOGGGGEAGGVVETGTESEI:PPKEKLAPEOPEOBAEA 60
Qy 447 EELMKSREMCVSGGDHQTLDLSPEEKTLPKHPREGIVSEVEMLSQERIKVQSGPLKLF 506
Db 61 EELMKSREMCVSGGDHQTLDLSPEEKTLPKHPREGIVSEVEMLSQERIKVQSGPLKLF 120
Qy 507 SSSGKLKLSGKKQKQKRGGGGDEPEGEYOHITHESPESEDQKSGSSASSPEPETTTL 566
Db 121 SSSGKLKLSGKKQKQKRGGGGDEPEGEYOHITHESPESEDQKSGSSASSPEPETTTL 180
Qy 567 EKPGLPADQGEAEGETTSDGEKKRE---GITPMASFKNMTPKKRYVRPSESDEKEEL 622
Db 181 EKPGLPADQGEAEGETTSDGEKKRE---GITPMASFKNMTPKKRYVRPSESDEKEEL 234
Qy 623 EKVKSATLSTSTSVSEMODEVKTVEEQKPEPKRRVDTSVSWALLICVSSKKRARA 682
Db 235 EKVKSATLSTSTSVSEMODEVKTVEEQKPEPKRRVDTSVSWALLICVSSKKRARA 294
Qy 683 SSSDEGGRTIGGDSHRAEASKDEAGTDAVPASTODQOAGSSSPFAPGSPSEGG 742
Db 295 SSSDIR-GRPLTGGGQSGGQSRGRSRTDAPASTODQOAGSSSPFAPGSPSEGG 353
Qy 743 VSTWESFKLTPPKRKSCKLEEK--AEDSSVEQLSTEIPEPSREESVWS--IKKFIGRKK 799
Db 354 VSTWESFKLTPPKRKSCKLEEK--AEDSSVEQLSTEIPEPSREESVWS--IKKFIGRKK 413
Qy 800 KRADQKQEQATVEDSGPVEINEDDPNPAVPLSEYNAVEREKEMQAGTEL:POLLGAVY 859
Db 414 KQMGHQEQATVEDSGPVEINEDDPNPAVPLSEYDAVEREKEMQAGTEL:POLSCGV- 472
Qy 860 VSEELSKTIVHTVSAVVDGTRAVTSVEERSPSWISASTPELEHAGAGAMPVEEVTERK 919
Db 473 VSEELSKTIVHTVSAVVDGTRAVTSVEERSPSWISASTPELEHAGAGAMPVEEVTERK 532
Qy 920 DIIAETPVLQTLTPGKRAHDMVTSEVDTSEATATETSEALTEVTEASGAETT 979
Db 533 DIIAETPVLQTLTPGKRAHDMVTSEVDTSEATATETSEALTEVTEASGAETT 592
Qy 980 DMVASVQSLTSDPTTEATPVQEVESVLDTEEEERQTAIIQAVADVKVESQVPAQ 1039
Db 593 DMVASVQSLTSDPTTEATPVQEVESVLDTEEEERQTAIIQAVADVKVESQVPAQ 652
Qy 1040 TVOIRGSKALEVEEVEEEDSEVLASEKEKDVMPKGPVQFAGAEHLAQSSEGTGATPESLE 1099
Db 653 TVOIRGSKALEVEEVEEEDSEVLASEKEKDVMPKGPVQFAGAEHLAQSSEGTGATPESLE 712
Qy 1100 VPEVTADVHVATCCYIKLQQLMEQAVAPESSETLTDSETNGSTPLADSDTADGTQODET 1159
Db 713 VPEVTADVHVATCCYIKLQQLMEQAVAPESSETLTDSETNGSTPLADSDTADGTQODET 772
Qy 1160 IDSQSKATAAARQSOVTEEEAATAQKEPSTLPNNVPAQOEHEGEPGVDLEPTQOELT 1219
Db 773 IDSQSKATAAARQSOVTEEEAATAQKEPSTLPNNVPAQOEHEGEPGVDLEPTQOELT 832
Qy 1220 AAAPVPLATVEVQGEVVMWLDGEKKEQEVFVHSGPSQKRAADVTYSEVGVAGCGE 1279
Db 833 AAAPVPMQTEVQGEVVMWLDGEKKEQEVFVHSGPSQKRAADVTYSEVGVAGCGE 892
Qy 1280 KESTEVQSLSEEGEMETVEKRETKPEOVSEEGEOETAPEHGTGKPLUTLDMDS 1339
Db 893 KESTEVQSLSEEGEMETVEKRETKPEOVSEEGEOETAPEHGTGKPLUTLDMDS 952
Qy 1340 SERKALGSLGSGPSLPDQKACIEVQVOSLDTVTQTAEAEEKVIEYVVISSETGESPE 1399
Db 953 SERKALGSLGSGPSLPDQKACIEVQVOSLDTVTQTAEAEEKVIEYVVISSETGESPE 1012
Qy 1400 CYGAILLPKESKSATGHTLQHAEDTVPLGPSPQASPIPIYTPAPESTLHMDLOGEIS 1459
Db 1013 CYGAILLPKESKSATGHTLQHAEDTVPLGPSPQASPIPIYTPAPESTLHMDLOGEIS 1072

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Qy 1460 ASQRESEEBEDKPADGPPADGKESTAIEKVLKAEPELLELESKNKIYLVNIQTAVDQFA 1519
Db 1073 ASQRESEEBEDKPADGPPADGKESTAIDKVLKAEPELLELESKNKIYLVNIQTAVDQFA 1132
Qy 1520 KRETAPETHAVDSQTVQVAPCLDSEPRNRCWTKMKDAMKHPVPPREDLOYLTYLEAM 1578
Db 1133 KRETAPETHAVDSQTVQVAPMLRDSREPNRCWTKMKVAKMKHPVPPREDLOYLTYLEAM 1191

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RESULT 2

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US-08-769-309A-5
; Sequence 5, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Klauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,309A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5741890and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-309A-5

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Query Match          52.9%; Score 4274.5; DB 1; Length 1780;
Best Local Similarity 57.8%; Pred. No. 9,2e-255;
Matches 957; Conservative 187; Mismatches 402; Indels 109; Gaps 36;
Qy 1 MGAGSSTEORSPED--PAGSDTSEILVSGHGAPEAS--GAADDPADA--DPATKLPKNG 56
Db 1 MGAGSSTEORSPEDPPRESSSTPAPEPSSGGPSAELAPPTADPAIASDPATKLLQNG 60
Qy 57 QLSVNGVAEQGDVHVOEENQEQ-----EEVVDVEDVQRESEEDVREKDR 102
Db 61 QLTSTINGVAEQDELSTLOEBDLNGQKALNGQALNSQEEVEIVIEVQGRDSEEDVSERDS 120
Qy 103 VEDMANSTAVEDITKQGEETSEIIEQIPASENVNVEENVOAESAQANDVGKXKFPVG 162
Db 121 DEMARKSAVVDHIDDDGGEENRN--IEQIPSSSESNLEELTQPTESQANDIGKXKFPVG 179
Qy 163 FKFTYKDKNEKSDPYQVLLTVKKDEGEAEASVAGADHOEPVETAVAGSESASKESELKOS 222
Db 180 FKFTYKDKTERPDYQVLLTVKKDEGEAE---AGADHODPSL--GAGAAKSESEPKOS 234
Qy 223 TEKQEGTLKQEOSSTEIPLQAESDOAAEEBAKDEGEKEKEPKTSPESPSSPVNSETTS 282

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Db 235 TEKPEETLTKREOSHAETSPPAESGAV--EECKEEGEKQEKEPKSAESPTSPVTSQTS 293
OY 283 SEKKFTTHMAGKRRKTSKKSKEDDLLEAKRKKEBAKVDEEKEKTPASEE-----337
Db 294 TTKKFTTQOMAKRRKTSRKPRKDEVEASEKKKEPEKVDTEEGAKAVKASE 353
OY 338 ----OEPADTDQARLSAAYEKEVPLEDOVGDLSEASEKCAPLATVEDEKMEALHO-E 392
Db 354 QAHPOEPASAHPRLSAAYEKEVLEPSEOVSSQSPSEKRAPLATVEFDEKIEVHOEE 413
OY 393 VVAENVHSTVEKTEEBEQGGGGEAGGVVEGTESLPPEKLAPOEVAPEAEELMS 452
Db 414 VVAENVHSTVEEBEQ-----KTEVEETAGVPAEELVGMDOAEPAEPAKELVKL 465
OY 453 REMCVSGGHTQULTDSPEEKLTPKHPREGIVSEVEMLSQERKRVGSGPLKTFSSGLK 512
Db 466 KETCVSGEPTQCADLSPEKVLTKPPEGVSEVEMLSQERKRVGSGPLKTFSTGLK 525
OY 513 KLSGKKQKRGKGGEDEGEYOHINTESPESADQKSGSSASSPEPEETTCLEKPLE 572
Db 526 KLSGKKQKGR--GGDEBEGEHTQVADSPDSQEBQKSSASSPEPEETTCLEKGLAE 584
OY 573 APQDGEAEGETTSDGKKREGITPMASFKKMVTPKRRVRPSESDKEELEKVKATLSS 632
Db 585 VOODGEAEGETTSDGKKREGVTPMAFVKMVTPKRRVRPSESDKEDELKVKATLSS 644
OY 633 TDSYSEMDEKVTVEEBOKPEPKRRVDTSVSMELICVSGSKARAKASSDDGGR 692
Db 645 TESTASEMOEEMKGVSEKPEPKRRVDTSVSMELICVSGSKARRRSSDDEGGR 704
OY 693 TIGDOSHRAEASKKEAGTDAVAPASTODODOGSSPEPAGSPGEGVSTWESFKRL 752
Db 705 AAGGQHQKADKAKKKEGTDTGLAGSQEHDEBQSSSPBQASPTBEGCVSTWESFKRL 764
OY 753 VTPRKSKSLKLEKAD---SSVEQLSTEIEPSRESVWSIKKFLIGRKKRQKQ 808
Db 765 VTPRKSKSLKLEKSEDSIAGSGVHSTPTDEKKEESWVSIKKFLIGRKKRQKQ 824
OY 809 ATVEDGPEINDDNNVAVVPLSFYNAVERKME---AQGTLPOLLGAVVSEELS 865
Db 825 APEEDGPTGAEDDSDVAVVPLSEYDAVERKMEAOQAQKAEOPBEOKAAVEVSEELS 884
OY 866 KTLVHTVSAVIDGTAAVTSVEERSPSWISASTPTEPLEHTAGAMPVEEVTXDLIA-E 924
Db 885 EGVVHMAAAVADGTAAATIIERSPSWISASTPTEPLEEYEAALITTEVLEEVIAEE 944
OY 925 EPPVLTQTLPEGKAHDHDMVTSEVDTSEAVTATETSEALRTEEVLEASGAETTDMVSA 984
Db 945 EPPVTEPLPENREARAGDTIVVSEALTPRAVTAETAGPLGSEGTAEASAETTEMVSA 1004
OY 985 VEOULDSPTTEATPVQVESGVLDTEEBERQTAILOAVADKVEEEOVAT-----1038
Db 1005 VEOULDSPTTEATPVQVESGVLDTEEBERQTAILOAVADKVEEEOVAT-----1064
OY 1039 -OTVORTGSALEKVEVEEEDSEVLASEKEKDMAPGVQEAQAEHLAOGSEFGATPS 1097
Db 1065 LQPVQGA-----EAPRPEQAEASGLKKEETDVVLKVDQAEKTEPFTQKVVGOTTPES 1118
OY 1098 LE-VPEATVADVDH---VATQV-----IKLOOL-MEOAVAPESSETLTDSENGSTPLAD 1147
Db 1119 FEKAPQVTESSISELVTTCOAETLAGVKSQEKVMEQAIPDSVETPDTSETDGTSPVAD 1178
OY 1148 SPDADGTODDITDSDSKATAAVRQSVYTEEAATAQKEEPTLPNNPAPQEHHEEG 1207
Db 1179 FPAFGTQDELEYEHEENEVHLV--PVKGTAEAVPAQKERPPA--PSSVVFQDETEEQSK 1236
OY 1208 -RDVLEPTQOELTAAVVPYLAQTEVQEGEVDMLDEKVK-----DEQEVFVSG--PNS 1259
Db 1237 MBDTLEHTKESVETVSLSTKEGTQ--EADQYADEKTKDVFFFGLSIDGTGTVSR 1294
OY 1260 QRAADVTYSEVGVAGCOEKESTEVOS-----LSIEGEMETDVEKERETKPEOVSE 1314

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Db 1295 EKVTEVALKGEETEAECRDDALELQSHAKSPSPVEREMVQVEREKTEAPETHNEE 1354
OY 1315 G--EQETAABHEGTYKRPVLTIDMPSSERKALGSLGSS--PLPPODKAGCTIEVQOSID 1372
Db 1355 KLEHETAVTVSEVSKQOLLQTVNVPILIDAKEVSSLEGGSPPLCGEEAVCTKIOVOSSE 1414
OY 1373 TTVTQTAEAVERKI--ETVVISSETGESPEVCYGAHLLPARKSSATGSHWTLQHAEDTVPLG 1430
Db 1415 ASFTLTAAAEKEEVAGVETNILETGETLEPAGAHVLEKSSKKNEDFAHNGCEDAVPTG 1474
OY 1431 PESQAESIPITVPAPESVLPDLQGEISASQERSESEEDKPDGADGKESSTALEKVL 1490
Db 1475 PDCQAKSTPVIASATTKKLSLSDLEGEKTSLSKMSDEVEQVACOEV--KVSALIEDL- 1531
OY 1491 KAPPE--LLELSKSNKIYLVNQTAVDQFART--ETAPETHAVDSOTQVPAQRDSEPN 1547
Db 1532 --EPENGILELETKSSKLVONITQVADQFVREETATETLSELOTQAHVIRKADSODAG 1589
OY 1548 RCWTK-----MKDAKKHHPQPREDLQVLTVLEA 1577
Db 1590 QETKEGGEPOASADDEPTITSKKESESTAVQQA 1624

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RESULT 3
US-08-994-570-5
; Sequence 5, Application us/08994570
; Patent No. 6090929
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nautel, Brian J.,
; APPLICANT: Klauack, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-994-570-5
Query Match 52.9%; Score 4274.5; DB 3; Length 1780;
Best Local Similarity 57.8%; Pred. No. 9,2e-255;
Matches 957; Conservative 187; Mismatches 402; Indels 109; Gaps 36;
OY 1 MAGSSTEORSPEQ--PAGSDTPESELVLSGHGRAAKS--GAADPRADA--DPATKLPQKNG 56
Db 1 MGAGSSTEORSPEQPPGSGSTPAEBPSPGSGPSAABPTADPAIMASDPATKLLQKNG 60

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;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
US-08-769-309A-3

Query Match          11.8%; Score 952.5; DB 1; Length 292;
Best Local Similarity 66.1%; Pred. No. 2.5e-51;
Matches 199; Conservative 30; Mismatches 53; Indels 19; Gaps 4;

QY 254 KDGEEKOEKPEPTSPSPSPVNSSETTSFFKKFPTHGNAGMKKTSFFKSKEDDLETAE 313
      1 KEEGEKOEKPEPKSASBPSTPVTSETGSTFFKFTQGAGMKKTSFFRKPEDEVEASE 60
QY 314 KRKEQEAKEVDEBEKETEPASEE-----QEPADPTDQARLSADYAEKVELPEDDY 364
      1 KKEGEKPEKVDTEEDGKAIVASEKLTASDAQHPQEPASAEHERRLSAEYKVELPEDEY 120
DB 61 KKEGEKPEKVDTEEDGKAIVASEKLTASDAQHPQEPASAEHERRLSAEYKVELPEDEY 120
QY 365 GDLEASSEKCAPLATEVDEKMEAHQ-EVVAEVHVSTYEKTEEDGGGGEABGVVVEG 423
      121 SGSQGPSEKPAPLATEVDEKLEVHQEEVVAEVHVSTVEERTEEQ-----KTEVEE 172
DB 121 TGSFLPEKLAEPQEVPOEAPEAEELMKSRMGVSGDHTQLDLSPEEKTLPKHPEGIV 483
      173 TAGSVAEELVGMADAPQZAEPAKELVKLETVCVSGEDPTQAGADLSPEDEKVLSPPEGVV 232
QY 484 SEVEMLSOERIKVQGSPLKLTFFSSGLKLSGKKOKGRGGGDEPEPEYOHHTESPE 543
      233 SEVEMLSOERMKVQGSPLKLTFTSTGLKLSGKKOKGR-KGGDESEGHVQPADSPD 291
DB 544 S 544
QY 544 S 544
DB 292 S 292

RESULT 5
US-08-994-570-3
; Sequence 3, Application US/08994570
; Patent No. 6090929
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Klauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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;
;      TOPOLOGY: linear
US-08-994-570-3

Query Match          11.8%; Score 952.5; DB 3; Length 292;
Best Local Similarity 66.1%; Pred. No. 2.5e-51;
Matches 199; Conservative 30; Mismatches 53; Indels 19; Gaps 4;

QY 254 KDGEEKOEKPEPTSPSPSPVNSSETTSFFKKFPTHGNAGMKKTSFFKSKEDDLETAE 313
      1 KEEGEKOEKPEPKSASBPSTPVTSETGSTFFKFTQGAGMKKTSFFRKPEDEVEASE 60
QY 314 KRKEQEAKEVDEBEKETEPASEE-----QEPADPTDQARLSADYAEKVELPEDDY 364
      1 KKEGEKPEKVDTEEDGKAIVASEKLTASDAQHPQEPASAEHERRLSAEYKVELPEDEY 120
DB 61 KKEGEKPEKVDTEEDGKAIVASEKLTASDAQHPQEPASAEHERRLSAEYKVELPEDEY 120
QY 365 GDLEASSEKCAPLATEVDEKMEAHQ-EVVAEVHVSTYEKTEEDGGGGEABGVVVEG 423
      121 SGSQGPSEKPAPLATEVDEKLEVHQEEVVAEVHVSTVEERTEEQ-----KTEVEE 172
DB 121 TGSFLPEKLAEPQEVPOEAPEAEELMKSRMGVSGDHTQLDLSPEEKTLPKHPEGIV 483
      173 TAGSVAEELVGMADAPQZAEPAKELVKLETVCVSGEDPTQAGADLSPEDEKVLSPPEGVV 232
QY 484 SEVEMLSOERIKVQGSPLKLTFFSSGLKLSGKKOKGRGGGDEPEPEYOHHTESPE 543
      233 SEVEMLSOERMKVQGSPLKLTFTSTGLKLSGKKOKGR-KGGDESEGHVQPADSPD 291
DB 544 S 544
QY 544 S 544
DB 292 S 292

RESULT 6
US-08-769-309A-17
; Sequence 17, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Klauck, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,309A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5741890and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-769-309A-17
```



```

1      SOFTWARE: PatentIn Release #1.0, Version #1.30
2      CURRENT APPLICATION DATA:
3      APPLICATION NUMBER: US/08/769,309A
4      FILING DATE:
5      CLASSIFICATION: 435
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Mr. 5741890and, Greta E.
8      REGISTRATION NUMBER: 35,302
9      REFERENCE/DOCKET NUMBER: 27866/33451
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 312-474-6300
12     TELEFAX: 312-474-0448
13     TELEX: 25-3856
14     INFORMATION FOR SEQ ID NO: 14:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 453 amino acids
17     TYPE: amino acid
18     STRANDEDNESS: single
19     TOPOLOGY: linear
20     US-08-769-309A-14

```

Query Match	7.9%;	Score 639.5;	DB 1;	Length 453;
Best Local Similarity	40.5%;	Pred. No. 8.7e-32;		
Matches 183;	Conservative 69;	Mismatches 165;	Indels 35;	Gaps 16;

QY	1110	VATCVQ-----IKLOOL-MEOAAVAPSSSEFLTUDSENSTPLADSDTADGTOQDEETISQ	1163
Db	6	VTTQCATLTAAGVAGSQEWMQMOLIPRPSVETPPIDSETLSDGSTPLADDACTGOKDEIVELH	65
QY	1164	DSKATAAVRQSYTEEAATAQKEEESTPLPNVPAQEEHGEPPG-RDYLEPTODELTAAGA	12232
Db	66	EENEEVHLV-VPGRTEEAADVPAQKERPPA-PSSFVFQEEETKQSKMEDTLHNDKSVSET	123
QY	1223	VPVLAKEVGEQEEVWMLQSEKK-----EEDQEVFHSQ-PNSOKADYTYDSEVMGA	1275
Db	124	VSLSTKTEGTO--EADQYADEKTKDVPFEEGLSGSDTDTIVSRKRVETALVKGSTEEA	181
QY	1276	GCOEKESTEVS-----LSLEEGEMETDYEKERETREKPEOVSEEG-EOETAAPHEHGYG	1329
Db	182	ECKKDALDELQSHAKSPSPSVREMYVQYREKRETEAPTHVNEKLEHETAVTSEESK	241
QY	1330	KPVLTLDMPSESEKGLDLSLGS-PSLPQDQKAGCILENOVOSLDTTYTQTAFAVEKVI-	1386
Db	242	QLQLOTVWVPIIDAKEVSSLEGSPPRCLOEAVCTKIDOVSEKSFULTAAEKEKVLG	301
QY	1387	ETVYVSTGSEPCVCGAHLIPAKSSATGSHMTLQHAEDTVLQEGSQAESPIIYTPAP	1446
Db	302	ETANILETGTLEPPAGHHVLEEKSEKNEKDFRAHGEDAVTPGDDCAKSTPIVYSKTT	361
QY	1447	ESTLHPDLOGELISASQRESEEDKDKDAPADPDGKESTALIEVKLAEPD--IILETSKN	1504
Db	362	KKGLSDLEGEKTTLSKKMSDEVDQVQAQEV-KVSAVIEDL---EPENGILELEFMS	416
QY	1505	KIVLVNTQTVADOPART-ETAPTAHYDSOTO	1535
Db	417	KLVNIIQTAVDQFVTEETATEMLTSELQTO	448

RESULT 9
 US-08-994-570-14
 ? Sequence 14, Application US/08994570
 ? Patent No. 6090929
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: Scott, John D.,
 ? APPLICANT: Naurent, Brian J.,
 ? APPLICANT: Klauack, Theresa M.
 ?
 ? TITLE OF INVENTION: Protein Binding Domains of Gravin
 ?
 ? NUMBER OF SEQUENCES: 24
 ?
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ?
 ? STREET: 6300 Sears Tower/233 South Wacker Drive
 ?
 ? CITY: Chicago
 ?
 ? STATE: Illinois

```

: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/994,570
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: NO. 609092sand, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/33451
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 453 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-994-570-14

Query Match 7.9%; Score 639.5; DB 3; Length 453;
Best Local Similarity 40.5%; Pred. No. 8.7e-32;
Matches 183; Conservative 69; Mismatches 165; Indels 35; Gaps 16;

```

```

Query Match      7.9%  Score 639.5  DB 3:  Length 453:
Best Local Similarity 40.5%  Pred. No. 8.7e-32
Matches 183:  Conservative 69:  Mismatches 165:  Indels 35:  Gaps 16:

QY 1110 VATCOV-----IKLOOL-MEOAVAPESSEITLDSSTNGSTPLADSDITADGTQODETISQ 1163
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 6 VTTQCAETIAGVKSQEMVMEQAIIPDSVETTPDSDSTPADDAQTGQKDEIVEIH 65
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1164 DSKATAVRQSQVTFEEKATQKEPSTLPLNNVPAQOEHEGEPG-RDYLEPTQOELTAANA 1222
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 66 EENEVHLV-PVRGTEAEAVPQAKERPPA-PSSFVQOEETKEQSKMEDTLLEHTDKDEVSET 123
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1223 VPLAKTEVGOGEVDMLDGEKV-----EQGEVPHVSG--PNSOKADVTYTDSEVMGVA 1275
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 VSIISTKTGCTQ-EADQYADEKTKVPPFEGLSGSIDGITVSRKRVTEVALKGCTEEA 181
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1276 GCOEKESTEVOS-----ISLEGEMETVEKEKRETKPEQVSEEG-EQETAPREHGTYG 1329
      | : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 182 ECKKDDALELGHSHAKSPSPYERENVQYVERKTKTAEPFLHVMEEKLLEHTATVSEEVSK 241
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1330 KPVLTLDMPSSERKALGSLGGS-PSLPDQDKAGCIEVQVOSLDTTYYQTATAEAVKVI-- 1386
      | : : : : | : : : | : | : | : | : | : | : | : | : | : | : |
Db 242 QLTQTVNPIIDIGAKEVSSLEGSPPCGLGOEAFCVKIQVOSSEASFLLTAAAEKVKLG 301
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1387 ETVVISEGESPECGAHLILAERKSATGCHMTLOHADDTYVLGPGESQAESPIITVTPAP 1446
      ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 302 ETANILETGETLEPAGALVLEEKSSKNEEDPAHHPGEDAVPTGPDCAKSPVIVSATP 361
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1447 ESTLHPDLQGEISASQRESEEDKPDAGCPADGKESTAIEKVLAEPE--LLEESKSN 1504
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 362 KKGSSDLEGEKTKTSLKMKSDVDVDQVACQEV-KVSAVIDL---EPENGILLETSS 416
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 1505 KIYLVNIOTAVDQFART-ETAPETHAYDSQTO 1535
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 417 KLYVNIITQAVDQFRTETATEMLTSLQTO 448
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 10
US-08-769-309A-15
; Sequence 15, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Klauack, Theresa M.,
; TITLE OF INVENTION: Protein Binding Domains of Gravin

```



```

APPLICANT: McKay, Ronald D.G.
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression as An Indicator of
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-JUN-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-853-913-2

Query Match          4.8%; Score 388; DB 1; Length 1805;
Best Local Similarity 21.3%; Pred. No. 1.8e-15;
Matches 319; Conservative 233; Mismatches 543; Indels 402; Gaps 75;

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Db 724 QESLSPSEEE---DOEAGSLQK-----ENOEPLGVEAEADOMLERLIEKESQSLK 772
Qy 323 VDEEEKETEPASPEOE-----PAEDTDARLSA-----DYKEVELPLE-- 361
Db 773 SPEENORICKPLERENQKRLYLENQETFPVLESNRQPLSLVEVEEQIVAPLEV 832
Qy 362 --DOVQDLEASSEKCAPLATEVFPEKMEAOEVAEVVSTVEKTEBOGGGAEGCV 419
Db 833 SQDSLGLS--AEENVQLR--YLEEDDCINKSLLE-----DKTKSLGSLERNRGS 880
Qy 420 VV-----EGTGESL--PPEK-----LAEPVEQAEAPAEILKSRMCVSGGDHQL 465
Db 881 IIPQESQVLSLRPEEDDRIVNHLKEKESQEFSSSEEEQVM--ERSLEGENHESL 937
Qy 466 TPLSPE-----EKLTPKHPGIVSEVEMLSOBRIVKQVSPKLKLSSSGLKLSGKKG 521
Db 938 SSVKEDQWESQLEKESQDSKSLSD--ESQTF-----GPLK--ENAEHLRLAQDQ-- 989
Qy 522 KRGGGDEEPGEYOHITHPESPESADEQKCESSASPEPEETTCLEKPLAPOD--GEAE 580
Db 990 -----BEQKLEQETQOTLRVAGNEQMAVSP-----EKVPELPKPLGNDQ 1030
Qy 581 EGTSDGEKKRGITPWPASFKNMVTPK--RYRRPSEDKKEELEKYS-----ATLST 633
Db 1031 EIASLSGKNOESIVSLKE--KGIEYVKSLETEIIEPLET--ABEDLERRKSIDTOELMST 1088
Qy 634 D---STVSEMODE---VKTGVEEOKP---EPPKRYVTSWEALICVSSKKRARA 682
Db 1089 EVARETVEPPEDEPPQSLSVDENRFTLSLKESEQLSLSKKNVETVEEDSOQLOVE 1148
Qy 683 SSDDGEGPRTL-----GDSHRAEASKDKDEAGTDAVPAST----- 719
Db 1149 EGIQEOHQESLREVYKQELPSSGNQORWEDYVGRKAVGEAPLATGVTGEDKAEHLRG 1208
Qy 720 ---QEDQDQ-----GSSSPRAGSPREG---EGYSTWSEFRRLVTPRK 758
Db 1209 QGEEFEAAAGELLQDIVEAASLSGSEPKQEVPAEALDNEGA-----LEVPAQ 1261
Qy 759 SKSLKEKAEAD--SSVEQLSTELIEPSREESWVSIKKFIIGRRKKRADGKQOATVEDSGP 816
Db 1262 SNEYTEREDEDRAQAGEQDSIEVTLGLEAKRTGEL-----EQEVVGLSD--P 1307
Qy 817 VEINEDDPNVPVAVPLSEYNAVEREKMAQNTPELLQGLAAVVS--EELSKTLVHTVSYA 875
Db 1308 RHFAREALRPS--LGESEVAKAKIQGLEPGKEPKKAGALDGLIELPKTSSSEALCO 1364
Qy 876 VIDGTAAVSVBERSPWSIASVTEPLEHTAGEAMPVEVEYKDIABET----- 926
Db 1365 GHEESESMEGWESEAS-----LETSDEHGSADAPQRPPEETEEDGAGQALTLAPQKLL 1418
Qy 927 -----PVLQTLPEGKDAHDMVTSE-----VDFSEAVTATETSEALRTEEVTEA 972
Db 1419 EPCSPPIIIT-----DHHEIQPAQEGIQEAGQWPEAGSEALERVENPEPGIGETIPG 1471
Qy 973 -----SGAETTDVMSVSQLTDSPTTEAATP---VOEVESGVLTDEEERQQTALIQ 1023
Db 1472 LDQMEGRRE-----SEADLGETLPDSTPLGLYLRSPASPKMDLAGFOR-----LS 1518
Qy 1024 AVADKKEE--SOVPATQTVQRTGSKALEKVEVEEDSEVLASEK-----EKDVPKRP 1075
Db 1519 POGDACKEDMGVAVPAQO-----GLSGPREEEEOGHGSDLSSEEDLGTASLLPGVP 1573
Qy 1076 VOEAGAEHLAQO-----GSETQQAIPESL--EVPVTVADVHVAT----- 1112
Db 1574 KEY--ADHVGOVPPVLIQPCMDQGESDGFADBEESGEGEEDADEGAEAGQAMWSG 1631
Qy 1113 -----COYIKLOLMEOQAAVAPSSSELTLDSTNGST-----PLADSDTADGTQOQETID 1161
Db 1632 ASGGCGKQVDIAGROGPVQESVGSGLMDGLRGAANPALEMSQDSAEBSGSES-- 1689
Qy 1162 SODSKATAAVROSQVTEEAATAQKEEPSTLPNNVPAQEHGEBEPGRDYLEFTPOELTAA 1221
Db 1690 ---ESASLLEGEGQVYTDH--LDAPQEVTSMPGVGDAFDIGQSPMLD----- 1732

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Db 2938 ---NRKNAILKLVSDTQEAIIINGYPDATEDELOANSKLINKILLDAKKOIGLARTNN 2994
OY 1545 EPNRCWTMKDAKMKHPVQPPREDLOVLTVLEAMAO 1580
| : : : | : : : | : : : | : : :
Db 2995 EYDDIYNEYSQ-KMKTIIPRVDTKAVARSYLNALAK 3029

RESULT 15
US-08-466-390-4
: Sequence 4, Application US/08466390
: Patent No. 5686562
:
: GENERAL INFORMATION:
: APPLICANT: YOUNKATLY, GARY
: APPLICANT: LIDGARD, GRAHAM P
: TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
: TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESS: TESTA, HORWITZ & THIBEAULT
: STREET: 125 HIGH STREET
: CITY: BOSTON
: STATE: MA
: COUNTRY: USA
: ZIP: 02110
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,390
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: PITCHER ESO, EDMUND R
: REGISTRATION NUMBER: 27,829
: REFERENCE/DOCKET NUMBER: MTP-013
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 248-7000
: TELEFAX: (617) 248-7000
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2101 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-466-390-4

Query Match 4.5%; Score 361.5; DB 1; Length 2101;
Best Local Similarity 19.6%; Pred. No. 9,6e-14;
Matches 364; Conservative 292; Mismatches 668; Indels 529; Gaps 81;

```

```

Db 641 ---AOREKAELSRKVEEIOACVETAROEQHEAOAVAELEIOLRSEOOAKTEREVAOER 697
| : : : | : : : | : : : | : : : | : : :
OY 345 DOARLSADVEKVELPLEDOVGDLEASSEEKCAPLAFVEYDEKMEAHQVAVAV-----H 398
| : : : | : : : | : : : | : : : | : : :
Db 698 DQ--LOEQLOALEKSLVKTYSLE--BEK--RRADALEBOORCISLKAETRLSEVOH 750
| : : : | : : : | : : : | : : : | : : :
OY 399 VSTVEKTEEEEOGG-----GGAEAGGVVVEGTGESIAPPEKLAEPQ-----437
| : : : | : : : | : : : | : : : | : : :
Db 751 KREKRELEERERAGRKLEARLLQLEBAHQALETVLRRELAEMAQHTFESCEQULYEV 810
| : : : | : : : | : : : | : : : | : : :
OY 438 -----EVPQDAEP-----AEELKSRKMCVSGGDHTQTLDSPEKTLPKHPBGIVS 484
| : : : | : : : | : : : | : : : | : : :
Db 811 AAMRDGYEDSOOEAOYGAAMPQEQIMTLKEBEKAROELQ-----BAKEKV-----AGIES 861
| : : : | : : : | : : : | : : : | : : :
OY 485 EYEMLSOORIVQSGPIKLFS--SSGLKLSGKKQKRGCGGDEEERGEVYHITESP 542
| : : : | : : : | : : : | : : : | : : :
Db 862 HSELQISRQONK-----LAELHANLARALQVOEKEVRQK--LADDJSTLOEKMAATSK 914
| : : : | : : : | : : : | : : : | : : :
OY 543 ESADQKGESSASSPEEPETTCLE--KGPLEA---PDQGAEBGTSSDGKKREGITP 596
| : : : | : : : | : : : | : : : | : : :
Db 915 EVA---RLETLYRKAGEOQETASRELVPKPARAGDRQPEMLEOOG-----RQFCST 963
| : : : | : : : | : : : | : : : | : : :
OY 597 WASFKMVTPKRRVRRPSSDKEE--ELEKVSATLSTSTVSE--MODEVKTGEE 650
| : : : | : : : | : : : | : : : | : : :
Db 964 QALQAM-----EREAOMGNLELRLAALMESOGQOQOERGOQOERVARLTQE 1012
| : : : | : : : | : : : | : : : | : : :
OY 651 QPPEEKRRVDTSVSWALICGSSKKRRKASSSDDEGPTLGGDSHRAEASDKC- 709
| : : : | : : : | : : : | : : : | : : :
Db 1013 RGRADQDLALEKRAARELEMRLOALNEQVREFATQELAHAL-----TKEGDOEL 1066
| : : : | : : : | : : : | : : : | : : :
OY 710 ---AGTDAV-----PASTQDQDQAGSSSPGAPSGSGEGVSTWESF 749
| : : : | : : : | : : : | : : : | : : :
Db 1067 AKIRGLEAQIKLEBELRTVQKQLEKAKKEHAHSGAAGREPIGPPL-EAL 1125
| : : : | : : : | : : : | : : : | : : :
OY 750 KRLVTPRKKSLSKLEKAE-----DSYEQULSTIEPSRESWWSIKKF 793
| : : : | : : : | : : : | : : : | : : :
Db 1126 RAVESKLEQOCCQOQOQOASLRSLEAERASRAERSALETLOGOLEKKAQELGHSQAL 1185
| : : : | : : : | : : : | : : : | : : :
OY 794 IGRRRKRA--DGKQOQAVEDSGVEI--NEDPNPVAVPL--SENNAYEREMEMO 846
| : : : | : : : | : : : | : : : | : : :
Db 1186 ASQORELAFFRKVDHSAEDEMKAQVARGQOERKKSLSISLEEVSIIINROVLE 1245
| : : : | : : : | : : : | : : : | : : :
OY 847 GNTLELPOLIGAVYVSEELSKTLVHTVSAVIDTRAITSVEERSPMISASYTEPLEHTA 906
| : : : | : : : | : : : | : : : | : : :
Db 1246 G--ESKELKRLVMAESESQKLESCACC-----RQROQA-----1278
| : : : | : : : | : : : | : : : | : : :
OY 907 GEAMPVEEYTERKDIIAETPYVLTOTLPFGKAHDMVTSE--VDFTSEAVTATETSEA 963
| : : : | : : : | : : : | : : : | : : :
Db 1279 ---TVPELQNAALLCGR-----RCRASGREAKQRYVASENLRQELTQOARAEELQOE 1328
| : : : | : : : | : : : | : : : | : : :
OY 964 LRT--EEVTEASGAEEFTTMVSAVSQTLDSPTTEATFVQGVESGVLDTFEEBQTOAI 1021
| : : : | : : : | : : : | : : : | : : :
Db 1329 LKAWQDEKFFQKQDQALSTQD-----EHTSTQALVSELLPAKHLCOOLOAE 1373
| : : : | : : : | : : : | : : : | : : :
OY 1022 LQAVADKVEESQVATQTVQRTGSKALE-----KVEEVEDSEVLASE 1065
| : : : | : : : | : : : | : : : | : : :
Db 1374 QAAAEKRHHHELE---GSKQAAGGIRALLRAQRELGLILIRQKVAQOERTAQOLRAE 1429
| : : : | : : : | : : : | : : : | : : :
OY 1066 K-----EKDVPKGPVQDAGAE 1082
| : : : | : : : | : : : | : : : | : : :
Db 1430 KASYAEQLSMLKKAHGLLAENRGLGERANLGRQFLEVLDOAREKYYQVOLAFAVADAET 1489
| : : : | : : : | : : : | : : : | : : :
OY 1083 HLAQSGEQGATPESLEVEPVATVDVHATQCVITLQOLQMBQAVAPESSETLTIDSETNS 1142
| : : : | : : : | : : : | : : : | : : :
Db 1490 RLAEVQREAQSTARELEV--MTAKYEGA-----KVKVLEERQROEROKTLTAQVIELS 1541
| : : : | : : : | : : : | : : : | : : :
OY 1143 TPLADSDTDADGTQOD--ETIDSO--DSKATAAVRQSOVTEEFAATAQKEPSTLPNNVPA 1198
| : : : | : : : | : : : | : : : | : : :
Db 1542 KTLABSDQASKYQOQKRLKRVQAGGSEQOEAORFOALQELQALSQKQAA-----1593
| : : : | : : : | : : : | : : : | : : :
OY 1199 QEEHGEPEGRDVLPTQOELTAAAVPVLAKTEVGOGEVDMLDGKVKDEQEVFVHSGPN 1258
| : : : | : : : | : : : | : : : | : : :

```

Db 1594 -----EHYKIQMEKAKTHYDAKKOONQLOELRSLLEOLKE-----N 1631

Qy 1259 SOKADVTYDSEWVAGCOEKESTEV-QSLSLSEGEEMETDV---EKEKRETKPEQYSEE 1314

Db 1632 KELRAEAEERIGHILOQAGLTCTKEBEQTCRHLLTAQVRSLSLAQVAHADQQLRDLGKFQVA-- 1689

Qy 1315 GEQETAPEHEGTYGKPEVLTLDMP---SSERKALG-----SLGSPSLPD 1357

Db 1690 ----TDALKSRPEQAKQQLDLSDLSLSCBEGTPLSTSKLPRTPQPDGTSVPGEPASPI 1745

Qy 1358 QDKAGCIEVOYOSLD---TTVTQTAEV-VEKVIETV--VISETGESPE----- 1399

Db 1746 SQR---LPPRVESLESXYFTPIPARSQAPLESSLSDSLGDFVLDGGRKTRRSARRRTQIIN 1802

Qy 1400 -CYGAHLPLPAEKSSATGSHWTLOHAEDTVPLGPESQA-----ESIPITIVPAPESTL 1450

Db 1803 ITYMKKLDVEEPPDSANSSEYSTRSA-----PASQASLRATSSSTOSLARLGSPDYGNSA 1855

Qy 1451 HPDLOG--EISASQRESEEEEDKPDAGPDADGESTAIEKVLKAPE-----ILELES 1501

Db 1856 LLSLPGYRPTTRSSARRSQAGVSSGAP---GNSSEFYM-GTCODEPQQLDWNKRIAELOQ 1911

Qy 1502 KSNKIYLVNVIQTAVDQFARTETAPETHAYDSQTQVPACRLDSREPNRCWTMKMDAKKHP 1561

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Db 1946 DPOETLRASWOPIQIAEGTGITTRQOKRVSLLEPHOGPGTPESKATSCFPR 1998

Search completed: December 10, 2002, 00:19:45
Job time : 55 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 00:19:52 ; Search time 73 Seconds
(without alignments)
355.106 Million cell updates/sec

Title: US-08-978-277A-4
Perfect score: 8073
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Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5421.5	67.2	1346	9 US-09-902-432-2	Sequence 2, Appli
3	4294	53.2	1781	10 US-09-738-877-3	Sequence 3, Appli
4	462	5.7	1786	9 US-09-742-096-3	Sequence 3, Appli
5	429	5.3	2665	10 US-09-864-761-34248	Sequence 34248, A
6	407.5	5.0	2368	10 US-09-815-242-5635	Sequence 5635, Ap
7	407.5	5.0	1325	10 US-09-815-242-12389	Sequence 12389, A
8	388	4.8	1325	10 US-09-864-761-35612	Sequence 35612, A
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14	354	4.4	1618	9 US-09-963-875-1	Sequence 1, Appli
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16	339.5	4.2	2139	10 US-09-727-384-6	Sequence 6, Appli
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19	323.5	4.0	1907	10 US-09-785-770A-16	Sequence 16, Appli

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23	305	3.8	3158	10 US-09-815-242-12611	Sequence 12611, A
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37	266.5	3.3	1192	10 US-09-758-140-6	Sequence 6, Appli
38	266.5	3.3	1192	10 US-09-972-599A-6	Sequence 6, Appli
39	265.5	3.3	1192	10 US-09-789-386-2	Sequence 2, Appli
40	265.5	3.3	1192	10 US-09-893-348-23	Sequence 23, Appli
41	264.5	3.3	1043	10 US-09-946-805-4	Sequence 4, Appli
42	261	3.2	5795	10 US-09-815-242-12610	Sequence 12610, A
43	258	3.2	1907	9 US-09-832-292-39	Sequence 39, Appli
44	255.5	3.2	1776	10 US-09-841-132-179	Sequence 179, App
45	255	3.2	1140	12 US-10-124-557-104	Sequence 104, App

ALIGNMENTS

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RESULT 1
US-09-902-432-4
; Sequence 4, Application US/09902432
; Patient No. US20020160002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A 070156.0597
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/902.432
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1596
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-902-432-4

Query Match      100.0%; Score 8073; DB 9; Length 1596;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1596; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1381 AVEKVIETVVISETGBSPCEVGAHLLPAEKSSATGHWTLQHAEDTVPLGPESQAEIPI 1440
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; Patent No. US2002016002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; APPLICANT: Susan G. Jaken
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A 070156, 0597
; CURRENT APPLICATION NUMBER: US/09/902,432
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1346
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-902-432-2

Query Match 67.2%; Score 5421.5; DB 9; Length 1346;
Best Local Similarity 91.6%; Pred. No. 1,1e-229;
Matches 1098; Conservative 24; Mismatches 62; Indels 15; Gaps 7;

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Db 235 EKVKSATLSTSTVSEMODEVKVYGEOKPEEPKRRVDTYSWMEALICVSSSKKRAKRA 294
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      800  KRADKQEOATVEDSGPVEINEDDPNVPVPLSEYNAREKEMQOCTELPQLGAVY 859
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RESULT 3
US-09-738-877-3
; Sequence 3, Application US/09738877
; Patent No. US20020015970A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan
; APPLICANT: Wells, Stephen J.
; APPLICANT: Glynn, Richard
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS, AND MEI
; TITLE OF INVENTION: SCREENING FOR ANGIOGENESIS MODULATORS
; FILE REFERENCE: A-69806/DIB/JJD
; CURRENT APPLICATION NUMBER: US/09/738, 877
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; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,425
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/US 00/22061
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 1781
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-738-877-3

Query Match      53.2%; Score 4294; DB 10; Length 1781;
Best Local Similarity 57.9%; Pred. No. 2,6e-180;
Matches 959; Conservative 187; Mismatches 401; Indels 108; Gaps 35;

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      57  QLSVNGVAEOGDVHVOEENQOQ-----EEVYDEDVQOGESEDYREKDR 102
      Db      61  QLSVNGVAEOGDVHVOEENQOQ-----EEVYDEDVQOGESEDYREKDR 120
      103  VEDMAANSTAVEDITKQGOEETSEITQIPASENNVEKVOAEOANDVGRKVFVG 162
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      163  FKPTVKKDNEKSDPNVOLLTVKKDEGEAGASVAGDHOEPVETRAVAGSASKESELOS 222
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      283  SERKFTTHMAGMKRKTSTKSKSKEDDLTAERKREDOEAKVDEEKEKTEPASEE----- 337
      Db      294  TERKFTTHMAGMKRKTSTKSKSKEDDLTAERKREDOEAKVDEEKEKTEPASEE----- 353
      338  ---OEPADTQOARLSAYEKEVEPLDEPOVDLEASSSEKCAPLATVEFDKMEAHQ-E 392
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      393  VVAEVHSTVEKTEEBEOGGGEAGGVVVEGTGESLPPPEKLAEPQEVPOEAEPAEELMS 452
      Db      414  VVAEVHSTVEKTEEBEOGGGEAGGVVVEGTGESLPPPEKLAEPQEVPOEAEPAEELMS 465
      453  REMCVSGCHTQLTLSPEEKLPHKHPGIVSEVEMLSQERIKYQOGLTKLPSSGGLK 512
      Db      466  KETCVSGEDPTGADLSPEEKLPHKHPGIVSEVEMLSQERIKYQOGLTKLPSSGGLK 525
      513  KLSGKKOKKRGGGGGEPEGEYOHHTESPESADROKGGSSASPEEPETCLCKGPLE 572
      Db      526  KLSGKKOKKRGGGGGEPEGEYOHHTESPESADROKGGSSASPEEPETCLCKGPLE 584
      573  APDGEAEGETTSDGEKKREGITPMASFKKMYTPKKRYRPPESDKEEELKVKATLSS 632
      Db      585  VQDGEAEGETTSDGEKKREGITPMASFKKMYTPKKRYRPPESDKEEELKVKATLSS 644
      633  TDSVSEMODEVITYGEOGPEEPKRRVDTYSWELTICVSSSKRKARAKASSDDGGR 692
      Db      645  TDSVSEMODEVITYGEOGPEEPKRRVDTYSWELTICVSSSKRKARAKASSDDGGR 704
      693  TCGGSHRAEASKQKEAGTDVVPASTODQOAGSSSPSPGSPSEGGVSTWSPRL 752
      Db      705  AMGGHQKXDEGKXKXETGTDGILAGSDHPGQSSSPGQAGSPFEGGVTWSPFRL 764
      753  VTPRRKSKLEKAD-----SSVEQLSTEIPSEESVSTKRPFGRRKRADGQEO 808
      764  VTPRRKSKLEKAD-----SSVEQLSTEIPSEESVSTKRPFGRRKRADGQEO 808
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Dd	765	VTPRKKSXSKLEKSEDSIAGSVENHSPDPEKGEESWISIKKFIPIBRKKRRKPDGRQEO	824
Qy	809	ATVEDSGPEVINEDDPNVAVPLUSEYNAVEREKME--AOGNTLPPQLLGAIVYSEELS	865
Dd	825	APVEDAGCTGANEDSDSDVPAVPLUSEYDAVEREKMEAOQAKGAEOQPOKKAATEVSKELS	884
Qy	866	KTLVHTVSAVVIDGRATVTSVEERSPSMISASYTERPLEHTAGEAMPPIVEYTERKILIA-E	924
Dd	885	ESOVHMMAAAAADGRTAATIIIEERSPSMISASVTERPLEOVEAEALLTIEULEREVIAEE	944
Qy	925	ETPVLTOTLPEGKDADHDMDVTSSEVDFTSSEAVTATSETSEALTEEYTEASGAETTDWMSA	984
Dd	945	EPPTYTEPLPENREKRGDTVVSSEALTEPEAVTAAATAGPLGSEBETASAEFTTEWMSA	1004
Qy	985	VSQLTSDPTTEEATPVQVESGVLDTEEEERQOTALLQAAVADKVEESQVAPAT-----	1038
Dd	1005	VSQLTSDPTTEEATPVQVEEGVDPDIEOERKRTQEVLOAAVAKKESQSOLPGTGGPEDV	1064
Qy	1039	-QTVQRTSKALEKEVEEEDSEVLASKEKEDVMKGVQOEGAGHLLAOGSTGQATGES	1097
Dd	1065	LQPVORA-----EAREBEOGAESGLKEKEDVVLAKVDAQEKTEPFGKVVGGTPEBS	1118
Qy	1098	LE-VEEYADVDH-----VARTCOV-----IKLQOL-MEOAVAPESSETLIDSETNGSTPLAD	1147
Dd	1119	FEKAPQVYESIESSSLVYTTCQAEITLAKVKSQEMVMEQALPDSVETPIPDSETDSTYPAD	1178
Qy	1148	SDTADGTQOQDETIDSQDSKATPAAVROSQVTEEBEATAOKKEEPTLPLNNVPAQEEHGEERG	1207
Dd	1179	FDAPGTOQKDEITVEIHENEVASQSGSTGEAEPAPKERRPPA-PSFVFQPEFKEQSG	1237
Qy	1208	-RDVLEPPOQELITAAVAVYLAKTEVQGGEGEVDMLDGEVK-----EEOGVYVHSG--FNS	1259
Dd	1238	MEDTLEHTDKVESVTSVILSKTGETQ--EADQVADKTKDVPFEGLGSGIDTITVSR	1295
Qy	1260	OKAADVYTDSEVMGAGOEKSTEVOS-----LSLEGEMTQDVEKEREKTPROVSEB	1314
Dd	1286	EKVTEVALKGBETEEAECKKDDALDELQSHANSPSPVEREMVQVYERKTEAPRHVND	1355
Qy	1315	G-EOETAAPEHEGTYGKPYLLTDMPSSEKNGALGSLGGS-PSLPDQDKAGCIEVQSD	1372
Dd	1356	KLEHETAVTSEVSGSKOLLQVNVPIIDQAKVSSLSGSPPCLOGEAEVCTKIQVOSE	1415
Qy	1373	TTVYOTAAVKEVLT--ETVIVISETGESEPCVGAHLLPAKSSATGCGHMTLQHAETVPUG	1430
Dd	1416	ASFLLTFAAEKEKVYGETFANILLETGETLEPAOAHVYLEKSSSEKKNEDFPAHGEDAVPTG	1475
Qy	1431	PEOSQESPIIYTPAPESLHLDLOGEISASQRESRESEEDKDPADADGKRETAIEKL	1490
Dd	1476	PDCQKSTPIVVISATTKKGLGSLDGEKTTSLKMSXSEVDEBOVAAOEV--KVSVAIEDL-	1532
Qy	1491	KAEPK-ETLEESKSNKIVLVANTQTAVOFOART-ETAEETHAIVDSQOTQVPAACRLBSREFN	1547
Dd	1533	-EPENGILLEETEKSSKVLQNTIIQTAVOFVTEETAEATMLTSELQTAHVIAKDSQDAG	1590
Qy	1548	RCWTK-----MKDAMKHPVPOPRDDLOVLYLEA	1577
Dd	1591	QETKEGEPEQASADETTPITSAKKEESESESTAVGOA	1625
RESULT 4			
US-09-742-096-3			
: Sequence 3, Application US/09742096			
: Patent No. US20020155441A1			
: GENERAL INFORMATION:			
: APPLICANT: DRUIHE, PIERRE			
: APPLICANT: DAUBERSIES, PIERRE			
: TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES			
: FILE REFERENCE: 200773USODIV			
: CURRENT APPLICATION NUMBER: US/09/742, 096			
: CURRENT FILING DATE: 2000-12-22			
: PRIOR APPLICATION NUMBER: US 08/973, 642			
: PRIOR FILING DATE: 1998-02-06			
: PRIOR APPLICATION NUMBER: PCT/FR96/00894			

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      PRIOR FILLING DATE: 1996-06-12
      PRIOR APPLICATION NUMBER: FR 95/07007
      PRIOR FILLING DATE: 1995-06-13
      NUMBER OF SEQ ID NOS: 29
      SOFTWARE: PatentIn version 3.1
      SEQ ID NO 3
      LENGTH: 1786
      TYPE: PRF
      ORGANISM: P. falciparum
      US-09-742-096-3

Query Match      5.7%; Score 462; DB 9; Length 1786;
Best Local Similarity 19.2%; Pred. No. 4.8e-13;
Matches 325; Conservative 291; Mismatches 644; Indels 436; Gaps

QY      53      QKNGQLSSVNGVAEGDVHVOEENQEOG--EEVDEVDVGRESDYREK---DRVE---105
      ||:|:|      :|:|      :|:|      :|:|:|:|      :|:|
DB      95      QVNGELAS-----EEVKEIIDLLEEGNTLTESVDONKLNLEAEADIKENILLINIEPKE 149
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      106      -----MAANTAYEDITKDOQ---EELSEIIDIPASENNVEVMQPAESQANDV 153
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      150      NIIDLNNIIONQSEKQESSENVQVSDLEFNELLNSVDVNGEYKENILF--ESQVDDTI 207
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      154      FKVKFEKVFQFKYTKKQKNEKSDPTVOLITVKKDGECAEASV--GADHDQEPSFETAVGE 211
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      208      FNSLVK-----SYQEOQHNVKEKVEESVDENDDESVEEVNEVNEVNDGDSVASSVEE 261
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      212      S--ASKESELKOSTEKOEGTLKOE-----OSTEIPLOAESDQAAEE 251
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      262      SIASSVDSIDSIJEENAVPTVEIIVAPSVESVAPSVESVEENVEESVAENVEESVAE 321
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      252      EAKDGEQKQKQKPTKSPESSSSPVNSSETTSSFKFTFHGACHRRKTKSKKSKEDDLF- 310
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      322      NVEESVAENVEESVAENVEEIVAPTVEIIVAPTVEIIVAPSVESVAPSVESVEENVEE 381
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      311      -TAERKKEQAEKQDEEKEKTEPA---SEEOBPADPTDOARLSADVEKVELPLEDQVD 366
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      382      SVAEENVEESVAENVEESVAENVEESVAENVEESVAENVEEL-VAPTYEELVAPTVEI-- 438
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      367      LEASSEKCAPLATEVPDEKMAHQEVAAEYHVSTVKTTEEOGGGGEAGGVVECTGE 426
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      439      VAPSVESVAPSVESVEENVE--ESVAENVEESVAENVEES-----VAENVEE 485
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      427      SLIPEKTLAEPOEVAEPAEELKKSRRMCVSGGDHTQIDLSPEEKTLPKHPEGIVSEV 486
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      486      SV-----AENVEESVAE-----NVEESVAENVEESVAENV 515
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      487      EMLSSQERIKYQGSPIKLFSSGLKTLGCKKQKGRKGGGDEBPGGYQHIIHESPSAD 546
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      516      BEIYAPTYEELVAPTVEIIVAPSVESVA-----PSVEESVEENVEESVA 560
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      547      EOKGSSASSPEEP-----EETQTLKGLPAPDQGAEBGTTSDGKKREGITPMASF 601
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      561      ENVEESVAENVEESVAENVEESVAENVEEIVAPTVEIIVAPT-----BEIYAP--SVY 612
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      602      KMWTPKKRVRRPSSDKEEL--EKVKSATLSTDSIVSEMDEY--KTVGEQKPEEPKR 658
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      613      ESVAPS--VEESVEENVEESVAENVEESVAENVEESVAENVEEIVAPTVEIIVAP----- 665
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      659      RVDTSVSMREALICVGSKKRRKRAKSSDDDEGPRITLGGDSHRAE--ASKDKKAGTDAP 716
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      666      -----TYEELIIVAPSVESVAPSVESVEE-----NVEESVAENVEESVAENVE 708
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      717      ASTOEDQDQAGSSSPSPAGSSPEEGYSTWESFKRLVTP-----RKSKSKLLEEKADS 770
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      709      ESVAEENVEESVAENVEEIVAPTVEIIVAP--PTVEIIVAPSVESVAPSVESVEENVEES 766
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      771      SVEQLSTEIERSREBSWVSIIKFTIPGRKKRRADKQDA--TYEDSGPVEINDDPNVA 828
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
DB      767      VAENVEESVAENVEES-----VAENVEESVAPTVEIIVAPSVEE-----S 806
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|
QY      829      VPIIETNAVEREKMEAGNTELPOLLGAVYVSELSKTLVHTVSAVINDGTRAVTSVE 888
      ||:|:|      :|:|:|      :|:|:|      :|:|:|      :|:|:|

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Db 807 VAPSVESVAVNATNLSDNL-LSNLLGI-ETEEIKDSILNELE-----EVKE 853
Qy 889 RSPSWISASTEPLEHTAGAMPVEEYTPKDIIAETPLVLTOTLPBG-KDADDMVTSE 947
Db 854 N---VTTILLEVEETTAASVTFPSNILEE---IDENTTNDTIEEKLIELHEMVL5AA 906
Qy 948 VDFTSAVTATETSEALRTEEYTEASGAETDMVASVQ-----LTDSPDTTEAT 999
Db 907 LENTOSEEEKKEIDYI--EVEKE-----EVATLLIETVEBAEKSANTTITEINLEF-- 958
Qy 1000 PVOEVESGLDTEEBERQOAILQAAVADKYKEESQVAPATQVORTGSKA-----LEKVEE 1054
Db 959 --NAVSENVAVNLEKLNFTVFNVLADKVEETVEISGESELENEMDKAFSEIFDVK 1016
Qy 1055 VEED-----SEVLASEKEKV-----MKG-----PVQ 1077
Db 1017 IOENLLTGMFRSTIETSIIVIOSEKVDLNENVSSIIDNIENMKEGLNKLKLENISSTEGVQ 1076
Qy 1078 EAGAHLAOG-----SETCQATPESLEVPVTAADVHVATCOVIK-- 1117
Db 1077 EYTEHVEQNVYDVVPAKQOFLGILNAGLKEMFLEVEFKSESQVITVEELKDE 1136
Qy 1118 -LQOLMEQ--AVAPSETLIDSEFNGSTPLADSPDADGTQDETIDSDSKATAVARQ 1173
Db 1137 PVOKEVEKETVSIIEEMEEINIVLEEEKEDLTDK-MIDAVESEIETSSDSKETEESIKD 1195
Qy 1174 SQTEEAATPAQKEEPTSLPNPNVPAOEHEGEGCRDYLE--PVOELTAAPVY----- 1225
Db 1196 K---EKDVLVVEE-----VODNMDSEVEKYLEKKNMEELMDAVBINDITSK 1242
Qy 1226 -LAKTEVGEGEVDML-DSEKVE-----BOEVFVHSGPNSOKAADVTYD-----SE 1270
Db 1243 LIETQELNEVEDLIDKMEKLEKALSEDSKEIIDAKDOLLEKVEIEHEHITTLDE 1302
Qy 1271 VAGVACQOE-----KESTEVOSLSLEGE---METDVEKKERET 1306
Db 1303 VVELKQVEDKEIEKYSDLKDLLEDILKEVEKEIELSEIILEDYKELKTJETDILEEKKEI 1362
Qy 1307 KPEQVSEGEQETAPAEHGTGYPVLTLDMPSSE----- 1341
Db 1363 EKDHPEKFEFEAEIKDLADILKEVSSLEVEBEKLEEVHEIKEEVEHIISGDAHIKGL 1422
Qy 1342 -----KQKALGSLGSPSLPDQKACIEVOVOSLDTTVOFAEAVEKVIETVY 1390
Db 1423 EEDDLVEYVDLKGSLIDMLKGMELGDMK-----ESLEVTYTKLBERVBS-LKDV 1473
Qy 1391 ISETGESPCVGAH-----LL-----PAEKSSATGGHMTLQHA--DTVP 1430
Db 1474 SSALGMDDEOMKTRKKAQRPKLEEVLLKEEVEKEPKKITKKKVRPDIDKPEKDEI-VE 1532
Qy 1431 PPSQAESITIIYTPAESTLHPDLQGEISASQRESEEDKPDAGPDADGKESTALEKVL 1490
Db 1533 VMKDEDI-----EEDVEEDIEIEDKVEDIDEDIDIGDKD---EVIDLIV 1580
Qy 1491 KAPELLELESKNKI 1506
Db 1581 OKERIEKVKAKKKL 1596

RESULT 5
US-09-864-761-34248
; Sequence 34248, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
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; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34248
; LENGTH: 2655
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034555.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 12
; OTHER INFORMATION: EST HUMAN HIT: AU117052.1, EVALUOE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P08640, EVALUOE 3.00e-10
US-09-864-761-34248

Query Match 5.3%; Score 429; DB 10; Length 2655;
Best Local Similarity 19.6%; Pred. No. 2,1e-11;
Matches 372; Conservative 270; Mismatches 755; Indels 504; Gaps 83;

Qy 9 QSPEDPAGSD-----TPSELVLSGHGPAEASC-----AAGPDADDPAT- 49
Db 301 QVSTPEPAKSDSLKESVBMKVPEKEGLSSHEVEKEGRKLARKHLKPEOPADGVSAVD 360
Qy 50 --KLDPKNGOLSVYVAGQGVHVOEENQGOEEYVDVEDVGQRESEYRREKDRVEEMA 107
Db 361 LEKLEARRRRFSDSNIKAKKQRPYAKKSPPEMDARVL-----SKQPVSSREYV---- 411
Qy 108 ANSTAVEDITKQGOETSEIIEQIPASENNVNEVQPAESQANDVGFKKVFFVGFKFTV 167
Db 412 -----LLRGEAEARRKVRKEILLKRES-----KTI----- 435
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTED for Windows Version 4.0
; SEQ ID NO 5635
; LENGTH: 2368
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-5635

Query Match      5.0%; Score 407.5; DB 10; Length 2368;
Best local similarity 17.5%; Pred. No. 1.6e-10;
Matches 317; Conservative 293; Mismatches 663; Indels 541; Gaps 71;

QY 47 PATKLPQKGLSSVNGVAGQGVHVOEERQEOEE- EYVDEVGORESDVEKED---- 101
DB 677 PTYKPOAKDDIIQAVTTTRKQO----- IKSNASLQDERKVANDKIGIKETKAKIDDAATT 732
QY 102 RVEEMANSTAVEDITKDGQ----- EETSEI----- IEQIPASNNVEEAVQPAESQ 148
DB 733 MNOVEAIKTKAIDINQIOTAPATTAKAAALEEPPEVVOAQIDQAPLNPDTTNEEVAER 792
QY 149 AN-DVGFKKVFKEVGFETVKKKNEKSDVQLT----- VKKDEGEAGASVAGDHOE 202
DB 793 INAKVSGVKAIEATTJAQDLERVKNEISKIENITDSTQTKMDAYNEVQAATARTQN 852
QY 203 PSVETAVGESASKESELKOSTEK----- QEGTLKQOSTE----- IPLQAESDQ 247
DB 853 ATVSNNTNEEVAADAAVEAQOGHLIDIOVYKSKQEVADTKSKVDKINAIOGQAKVVP 912
QY 248 AAEEEAKEDE-GEEKQKEPPTKSPESPSPVNESETTSFKFFKHGNAWKKTSFQSK- 305
DB 913 AADTEVENNYNRKQIOTIS----- NASTTEKQAAIT----- ELDTKKQEA 954
QY 306 ----- EDDLETAE----- KRKEQAEKVDDEEKET----- EPAS 335
DB 955 RFWLDAANTNSDVTAKONGIAINQVQATTKKSDAKAEIAQKASERKATIEAMNDSTT 1014
QY 336 EGEPEAPED-TDQARLSADVEKVELPLEDOYGDLEASSEECA----- PLATEVFDE 385
DB 1015 EEOQAQKDVQDAVVATAMADIDNAANTDVDAKNTNEATITAITPDANVYKPAKQAID 1074
QY 386 KMEAHQEVVAEIVSTVEKTEERQGGGEGGVVEGEGSELPRPKLAEPQVQEAER 445
DB 1075 KYQAQETAIT----- DANNCATTE----- EKAAKQOVOTEKTT 1107
QY 446 AEELMKSRMCVSGDHTQLTDLSPREKTLPHHEGIVSEVEMLSQERIKVQGSPLKUL 505
DB 1108 ADTAI----- DGAHTN----- AEVEAKNAEIAKIEAIIQPAIT 1140
QY 506 FSSSGIAKISGKKQKRGCGGDEDEGEYOHITF----- S 541
DB 1141 TYDNAQQAATATANERKTA----- IAQTQDITAEIIAANANVDAVTOANNITEANS 1194
QY 542 PESADEQK--GSSAS--SPEEPEETTC--EKGPLAPQDGEAEGETSDGKKREGIT 595
DB 1195 QNDVDQAKTTGESIDQVPTVYAKKATAVTDKANNITTAITDONGVPTADAGKNSIQSIQ 1254
QY 596 PNASEFK----- MVTPKRRVRPSESDEE----- 620
DB 1255 PATAVVSNKANDVDQAVTQNOAIDNTGATTEKNAKADVLKAKERAYQDILNAQTIN 1314
QY 621 ELEKVSATLS----- STDSVSEM-QDEVKTYGEEK----- PEPRRRVD 661
DB 1315 DVTQIDQADVADVOGITADTTIKDKVAKDELATKAREQKALIAQFADATTEEREQAOQVVD 1374
QY 662 TSVSW----- EALICGSSKKRARKA----- SSSDEGEGPT----- LG 695
DB 1375 AELTQGNONIEENAGSIDVNTAKDNAIQAIIDPQASTVKTNAKRALLETMONKITEIILN 1434
QY 696 GDSHRAEASKD----- KEAGTDAVPAST----- QEOQOAGSSSSPEPAG 735
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DB 1435 NNETNEEKNDIGPVRAAYEEGLNINNAETTGDTTAKDTAVKQOQLHANPVKKPAG 1494
QY 736 SPEEGEGVSTWESFKLVLPPRKKSKSLEKAL-DSSVEQLSTIEPSPRESVY----- 788
DB 1495 KTAIDQAAAD-KTQIQEQTTPNASQOEINDAKOEVDELNAQKTNIDQSSIDEVDAVRE 1553
QY 789 ----- SIKKFIPIGR----- KKRAG 804
DB 1554 GKAKINAVKTFSEYKDDALAKIEAAINAVTEADNSNASTSSIEAKKQKLAELKQTAQ 1613
QY 805 KQOATVEDSGPVEINEDDPNV----- PAVVPLSEYNAVEREKMAQGNTELQ 853
DB 1614 NVNQAATSKDIDIEVQIHNDLDINIDYITPGKKSATTDLYAVADQKKNISATNTAQE 1673
QY 854 LICAUVSEBELTLVHTYS----- VAVIDGTRAVTSVEERSPSWISASY 898
DB 1674 KQQAIRQOVQNOVTALESINGVDNDVDALTOGKAALIDALIOVDATVPRKANQVIDAKA 1733
QY 899 TEPLF----- HTAGAMPVEEVTE--KDIIAEETPV--LTQTLPEGDAHDQV 944
DB 1734 EETKESIDSDQLTAEKTEALAMIKQITDOAKOGITTDATTAEVKAKAQGLEAFDNT- 1792
QY 945 TSEVDTSEAVTATETSEALRTEEVTEASGAETTD----- MVSAYSQLTDS 992
DB 1793 --QIDSTEKQKALELEETLALDQIEAGVNDADATTEKEKAFNALBIDLSKATEDISDQ 1850
QY 993 DTTEEATPVQEVSSGLDTEEBERQTAI----- LQAVADKVEESQV----- PATQV 1041
DB 1851 TNAEIAI----- VNSALEDLQAKRINPVYKKNALREIVYNAQIEIINNADADAKEI 1906
QY 1042 QRTG----- SKALEKVEEVEDESEVLASEKEDVMK----- GPVOAGAETHAOGSE-- 1089
DB 1907 ARTDLOGRYDRPADKIDKQNTIEV--AELOAVTITAEIAYIPQNDPNANDTRNGSGDND 1964
QY 1090 ----- TGOATPESLEVEPVATADVAVATCOVITLQOLMEQAVAPESSETLTJSETNGSTP 1144
DB 1965 ATANSANATPENTGQPNVTESTDNANA----- DTSSTTNNQNOAAG 2008
QY 1145 LADSDTADGTQODETID--SODSKATAAVROSQVTEEBATAOKKEPSTLPNN----- VPA 1198
DB 2009 ETTATSNASSATDANDKDRQOANNSSADSTSNPTMDNVTSTKPEVEST--NNGTTDKPA 2066
QY 1199 QEEHGEPEGRDYLE----- PTOELTFAAIVPLAKTEVGOBQBEVMDQEKV 1246
DB 2067 TEADNATPESATNNSTTATNENAPTESTATA--PTTAST--GAESSADSKOASVY 2121
QY 1247 E-EQEVFVHSG----- PNSQKADAVTYDSEVNGVACQKESTEVOSLSLEEG 1293
DB 2122 DSKQNAEVENNNSAESQSTNGKVAQPKSENKAKAKKQGRDSTNGSMVESTETETLPSADITEP 2181
QY 1294 EMETDVEKEKRETKPEQVSEE--GEQETAAPHESTYG----- KVLVILDMPSER 1342
DB 2182 KYSSNNTSKKEESTTSQTDAEQHSNDTNYVNSMEADSESNVDIVSNKP--STSKPSEAK 2239
QY 1343 GKALGSLGSPSLPDQDKAGCIEVQVOSLDTVYTORAEAVEKIEVIVVISTEGSESPCG 1402
DB 2240 DKA----- TSEDSQKADMATADTKNOASIGATADVNNKATQ------- DG 2280
QY 1403 AHLIPAKSSATGAWTLOHAEDTVPLGPES--QAESIPIIVYPAPESTLHPDLQGEISAS 1461
DB 2281 ANASPA----- TVSKGGSANAMQDLVNTKTKENKANKASQOQGVN-- 2321
QY 1462 QRESEFEEDKPDAG 1475
DB 2322 -KPKQAQKTLPTG 2334

RESULT 7
US-09-815-242-12389
; Sequence 12389, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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Db 652 TEN-----GORTPFAN-----EKTSSPAEPTHEGERTPLANENTTISPAPTEMR 697
Qy 841 EKMEAGNTELPOLLGAVYSELSKTLVHTVSVAVIDGTRAVTSVEEESPWISASYTE 900
Db 698 ETTANEKTPPP-----AEPTEMRERNTENTTP-----SPAQ 730
Qy 901 PLEHTAGEAMPVEEVEETEDKIIAEETPVLTQTLPEGKAHDMDVSEVDPTSEAVTAET 960
Db 731 PTEN--GDRTPLANEKT-----TPSLAEPTENG-----RTFPAEKT---S 768
Qy 961 SEALTEEVTASGAETTDWASVQSLTSDPTTEEATPVOEBSGLVLTDEEERQTOA 1020
Db 769 SSAFEPTHEAERTPLANENT-----TSSP-----AEP-----TENREBTAN- 803
Qy 1021 ILQAVADVKKESSQVPAQVQORTSKALEKY-----EEVEEDSEVLASKEKDVPKGV 1076
Db 804 -----EKTQPPAEPTENRE--STANEKTPPAEPTREMTANE--NTTISPAPET 852
Qy 1077 QGAGAEHL-----AGSETGOATPESELEPEVTADVDHATCQVAKILOQMEQAVA 1127
Db 853 EHEEHTPLANETKTLSPAEPTENGERTP-----FTNEKT 887
Qy 1128 PESSETLIDSETNGSTPLADSDT---ADGTOODETIDSQDSKATAA--VROSOYTEEBA 1181
Db 888 PSSAE--PTEHGERTPLANEITTPSRAEPTHEGERIANEKAETPSAKPTEHGETTVNED 944
Qy 1182 ATRQKEEPTLNNVP-AQE-----EHGEERGRVLEPTQOELTAAPVPLAKTE 1230
Db 945 TTPSSAEPTENGERTPLANENTTSPTESTEGERTANKTTPSPAEPTE----- 994
Qy 1231 VGOEGEVDMLDEKYEEOEVFVHSGPNQKADVTYDESVAGVAGCCEKSETEVOISL 1290
Db 995 -----HEERTPSANEKTIIPSAKPTHEHEMTPSA-----NEMTTPSPVAP 1034
Qy 1291 EGEHEETDVEKRETKRPQVSEEGEOETAPBH--EGTYGKVLTLDMSSRGALGSL 1349
Db 1035 TFGHKRTTLANKITLSPGPTFHGAKTTSANEKITPPLAKPTEHGERTSPNDKITS- 1093
Qy 1350 GGSPLPDODKAGCIEVQVOSLDTTV---TOTAAVEKIEIVVISEGESPECGAHL 1406
Db 1094 -AAESTEHDRKTSANVTTPAPAEPIKAHAKRTTLAHEK--TOVTEKSTHEPKETS--- 1147
Qy 1407 PAKSSATGHTLQHAEDTV-----PLGPSQAESI-----PIIVTAPAE 1447
Db 1148 TTEKTRPRPEKPTL-YSEKTICTKGKMPV--PEKPTENGNLTTLTEIKAVKSTENE 1205
Qy 1448 STLHPDLQGEISASORESEEDKPDAGPDADGESTALEKVLKAPPELLEESKNKIV 1507
Db 1206 KT-----AAVTKIKPSVKVTGDKSLTTSSTHNTKE--VTHQVPTGSFT 1248
Qy 1508 LNVITQVADQFARTEFAPETHAY---DSQTOVPACRLDSREPNRCW 1550
Db 1249 LITSRKLSITSEATGNESHPLNKGSGKIHAGOMGENDSFPRAW 1295

RESULT 9
US-09-971-536-70
; Sequence 70, Application US/09971536
; Patent No. US2002015976A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Lubbers, Mark
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul
; APPLICANT: Reid, Julian
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Methods
; TITLE OF INVENTION: Using Them
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; FILE REFERENCE: 1043c2
; CURRENT APPLICATION NUMBER: US/09/971,536
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCF/N201/00160
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 70
; LENGTH: 1879
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-971-536-70

Query Match 4.7%, Score 382, DB 9, Length 1879;
Best Local Similarity 19.1%, Pred. No. 1.6e-09;
Matches 324; Conservative 302; Mismatches 726; Indels 342; Gaps 70;
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Qy 20 TPESELVLSGHGFAAASGAGADPADADPATKLPQ-KNQLSSVNGVAEOG--DVHVGEE 75
Db 124 TATERAKQKQDGVAAEATYAKAAIDQAQETEGVQARDAGIAIDQHOPTGGLNREEA 183
Qy 76 NQEGQEEV---VDEDVQGRESEDEVREKDRVEEMAANS--TAVEDITKQGOEETSETIE 129
Db 184 KAIIDAEAKYATLEIDQBSTLATSSEKAQKQGVADAEAKAKATAID-----QAOTILEID 237
Qy 130 Q-----IPASENNVEENV-QPAESQANDVGKKYVK 159
Db 238 KAKDDGKAIIDAHQKAGDFDTRKAQAKDAIDAEAKYKDAIDQPTTLAKKTKQK--Q 295
Qy 160 FVGFKETVYKDKNEKSDPMYQOLLTVKKDEG--EGAEASVGAGH---QEPSVEPTAVESASK 215
Db 296 GVGDEATYAKTAIDAKTIDGVIQAKDDGKAIIDQHOQGTDLATRKOSAKAIDAEAK 355
Qy 216 -----ESELKOSTEKO-----EGTLQEOSSTEIPLOASDAQAEBAKDE 256
Db 356 ITDAINQDQTLSTERKDAQKQAVADEAKAKKAAIDQAOQNADAI-LQAQADGKAIIDAKHQ 414
Qy 257 GEEKQKEPTKPSPESSPVSSETTSSEKFFTHGMAGKRTSKTSKSKEDDLTAERK 316
Db 415 IGADLDQTKTKAKQA---IDKEEA---KVL-----ALIEDPTLTSARKK 453
Qy 317 EGEAEKVEDEEKEKTEPASEEOEPAPEDTQ--ARLSAD-----YEVKLPLEDVQDLE 368
Db 454 AQKQGVADETAKATAIDS-----ARNADELAKAQAADGKAIIDAQHRLGMDLAKKRTAQ 508
Qy 369 ASSEFKCAPLATEVDEKMEAHQEVVAEVHVSIVTEETEEQ--GGGGEAEGGVVE--- 422
Db 509 AAIIDAEAAVGAIDODPTLTLSQEKAAQKQTFVAETAKKDITAKAQAADGVYQAEKGI 568
Qy 423 -----GTGESLPPEPKLAEOEVPOEAEPAELKSRBMVSGGDHNO--LTLSPPE 472
Db 569 QAIDGQSGALLDTRKYDAKKAIDAEAKAINDAIDQVTLTSARKAKQKQVTEBAVKA 628
Qy 473 KTLPRHPEGVSEVEMLSQERIKYQGSPLKTLFSSSGIKTLGKKGKQKRGGGGDEEP 532
Db 629 KT-----AIDAAKNADIVDQAKASGLOAIDAIVHSG-TLLDTRKQDAK--AIDAEV 678
Qy 533 FY-----QHITHSEPSADQKGESSASSPPEPETTCLEKGPLAPDQGEAEGETTSDG 587
Db 679 KYIAAIGQDVTLTQAEKLTQQAQAVADAQO-----AKAIDAANKNADAVDQAKADG 729
Qy 588 EK-----KREGITPWPASFKNVTPPKRVARRPESDKEEELKVKSA---TLSSTDSV 637
Db 730 IKAIDAQHOAGL--ALNKRKEAAKKLI-----AETADKVAQAIGQDVTLTATOKAV 778
Qy 638 SEMQDEVKTVGEEQ-----KPEPKRRVDTSVSMELILCVGSSKKRARRAS 683
Db 779 QROAITVEVTKANQAIIDAGNADAVDAQKNAGVKAITYDHQSGOAL---ADRRKRDAR-Q 833
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Db 1110 TTADAIDAHTNAEVEAKKAAIAK--IEAIOPAT-----TTKD-----NAKE 1151
QY 603 MYTCKKRVRRSESDKEKELEKVKASATLSDTSVSEMODVKVTVGEQKPEEPKRRVDT 662
Db 1152 AIAATKAEKKAIAOTOTITAEETAAANADVMTQONNSIEAANSNDVDQATGTGEN 1211
QY 663 SVSWEALICVGSKKRKAASS-----DDEGGPRTLGSDSHRAEASKDKENGTD-- 713
Db 1212 SI--DQVTPYVKKATANEITAILNNKQELQATP-----DANDEEKQADAENGTENG 1264
QY 714 ----AVPAST--QEQDOAQSSPEPPAGSPSEGESVSWESFKRLVTPR--KSKSKLE- 764
Db 1265 KANQAISAATTNAQVDEKAKANA-----EAAINAVPKVVKQAQAKDEI 1307
QY 765 EKADSSVVEOLTELEPERESWVSIKKFIPIGRKKRADGQEQEATVDSQVPEINEDDP 824
Db 1308 DQDQATQTNVNNQONNATEKEKAI-----QQLATA-----VTDAKN 1345
QY 825 NVPAVPLSEYNAREKMEAGNTELPOLLGAVYVSELSKTVHTVSVAVIDGTRAVT 884
Db 1346 NITFA--TDDNGVDAQNDACKNSIQSTQPAFAVKSNAKNVDQAVTQONQAIQNTIGAT 1402
QY 885 SVBERSPWISASVTEPELEHTAGAMPVEVTEKDIIAETPVLTQTLPGKD-AHDDM 943
Db 1403 TEE-----KNAKADLVKAKERAYODIINAQT--TNDVTOIKDQAVADI 1444
QY 944 VTSEVDFTSEAVTATESEALRTEEVTEASGAETDMVASV-----SOLDSPTPTTEA 998
Db 1445 QGITADTTIKVAADELTKRAMEQALIAQTADATTEKEBQANQOVDAQLOQNONINIA 1504
QY 999 TPVOEVESGLDTEEBERQOTAI--LQAVADKVEESQVPAQTQVORTGSKALEVEVE 1056
Db 1505 QSIDVNTA-----KQNAIOAIDPIQASTD-VKTNARAEITLTEMQ-----NKITEIL 1550
QY 1057 EDSEVLASEKEDVMPKPVQVQACAEHLAQSGSEIGQATPESLEPEVYADVADHATCOYI 1116
Db 1551 NNNETNEKEKNDI--GPBRAAYEEGL-----NNINATTTGDDVTJAKDTPAVQ 1596
QY 1117 KLOOLMEQAV-APESSELTLDSEFNGSPPLADSDPTADSTOOD-----ETISQDSKATAA 1170
Db 1597 KVQOLHANPVKPKKAKELDQAAADKKTQI--EOTPNASQOEINDAKQEVTELNQATN 1654
QY 1171 VROSOVTEEEAATAQKEEPTPLPNVNPQOEHEGEEGRDVLPTQOELTAAAVPLYANTE 1230
Db 1655 VDQSS--TNEYVDNAVKEGAKI--NAVKTSEYKKD-----ALAKIE 1693
QY 1231 VQGEVDWLDGEKV-----KEQEVFVHSG----- 1256
Db 1694 DAYNAKVAEADNSNASTSSEIAEAKQKLAELKQADQNVNQATSKDDIEVOIHNDLNIN 1753
QY 1257 ----PNSOKA-----DVTYDSEVMVAGQKESEPEVOSTL----- 1288
Db 1754 DYTTPGCKKESATIDLYAVAOQKNNISADTNATODEKQOAIKQOVQOVJALAESINNGV 1813
QY 1289 -----SLEGEEMETDVEKEREKRETPP-----QVSEGEQOETAPEHEGTGKPVLTLD 1336
Db 1814 DNGVDQDALTOGKAIDAIDQVATVPRKANOAIKQVADPTRESIDQSDQ----- 1862
QY 1337 MPSSERKALSLGSGSPSLPQODKAGCIEVOVOSLDTTVTQTAVER-----VITFV 1389
Db 1863 LTAEEKTALAMI--KOITQOAKQGI-----TDATTTAA--VERAKAQGLEAFAPNI 1909
QY 1390 VISETGEPEVCVGAHLPAEKSSATGCHWTLQHAEDVPLG-----PESQASFI 1438
Db 1910 QIDST-----EKQAKIE--ELETTALDQIEAGVNNNAQDATTKEKEKFTNAL 1952
QY 1439 PIIVTPAESTLHPDLQELISASQERSESEEDKPDAGDAGKESTALEKLAKEPIL- 1497
Db 1953 EDLISKATEDISDQTTNMEINTVKNSALEQJLAKQKINPEVKNALAEALREVVNNQIEIIT 2012
QY 1498 --ELSSSNKIVLVNIQTAVDQFARTETAPETHAVDSOTQ---VPA 1538

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Db 2013 NADADASAKETIARTDLGRYFDRFADKLDKQTQTNAEVAELOWNTIPA 2058

RESULT 11
US-09-815-242--12967
; Sequence 12967, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12967
; LENGTH: 2478
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12967

Query Match 4.7%; Score 377; DB 10; Length 2478;
Best Local Similarity 18.3%; Pred. No. 3.6e-09;
Matches 305; Conservative 274; Mismatches 625; Indels 462; Gaps 68;

QY 47 PATKIPQKNGQLSSVNGVAEQDVHVOEENQOE- EYVDEDVQGESEDEVRKD--- 101
Db 681 PTVPPOAKQDIIQAVTTRKQO---IKKSNASLQDEKDVANDKIGKIEYKAIKIDIAAT 736
QY 102 RVEEMAANSTAVEIDITKQGEETSEIIQIPASENNVEEMVQAPESQANDGPFKKVRFV 161
Db 737 NAOVEAITKKAINDINOTTPATFTAK-----AAALEPDEYVQAOIDQ----- 779
QY 162 GFKFTVKKDKNEKSDVQOLLTVKKRDEG- EGAEASVGA GDHQPSEVETAVGESASESLK 220
Db 780 --PLNPDTTNEVAEALIERINAQVSGKALEATTNQD-----LEKKNKEISKIEINT 832
QY 221 QSTE-----KQEGTLKQESST-----EIPLOAESDQAAEBEAKDEG----- 257
Db 833 DSTQTKMDAYNEVQOAAARAKQONATVSNATNEV--A-AD- AAVPAQKQGLHDIOVV 888
QY 258 EKEKEKPTKSPSPSSPVNSETSSPFKFFTHWAGKMKTSFKKSQEDLTAERKKE 317
Db 889 KSKQEVADTKS--KVLDKINAIQT-----QAKYKPADVEVENAVYNTK 930
QY 318 QE-----AEKDEEKEKTEPEASEQEPADTDQARLSADYEKVELPLEDQVGLLEASSE 372
Db 931 QEIQNSNASTTEKQOATTELDTKQKEARTKLDANNSD----- 970
QY 373 EKCAPLATEVEDEKMEAHQEVVAEIVHVSVEKTEEBEGGGGGAEGVVGVEGTGSLPEPK 432

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Db 971 -----VTTAKONISIAINOVOAATTKKSDAKAEIAOKA---SEKRTAIEAMNDSTTEBQ 1021
Qy 433 LAEPOEPOEAEP-----BEIMKSRMVCVSGDHTOLT-----LSPREKTLPRKREGI 482
Db 1022 QAKAKDVDAVYANADIDNAANNV-----DNAKTTNEATIAITTPDANKVPAKAKOI 1076
Qy 483 VSEVEMLSSOERIKVQGSPLKLLSSSGLKLSGKKOKGREGGREGGEPREXOHIITEEP 542
Db 1077 ADKVQ---AOE-----FAIDGNNSTSTEBKAAKQOYOTEK 1109
Qy 543 ESADBECKGSSASSPPEPETTCLEKPLAPODGEAEETSTDSGKREGITPMASFKK 602
Db 1110 TTADADAIDAHTNAEVAAKKAIAK--IEAIOPAT---TTKDD-----NAKE 1151
Qy 603 MYTPKRRVRPSEDEKEELEKVSATLSTDSVSEMDEVTVGEBOQPEPKRRVPT 662
Db 1152 AITKANKNEKTAIAOTODITAEBIAAANDVDNAVYQANSNIEAANSQNDVDAKTGGEN 1211
Qy 663 SVSWEALIVGSSKKRARRASS-----DDEGPRITGGDSHRAEASKDEAGTD-- 713
Db 1212 SI--DOVTFYVNNKATARNETITAILNNKLOEIOATP-----DATBEKOAADEAMTENG 1264
Qy 714 ----ANPAST--QEOOQAGSSSPRAGSPSEGEVSTWSEFKRLVTPR--KSKSKLE- 764
Db 1265 KANOQISAATTAQAQDEAKANA-----EALINAVTPYVKKQAAKDEI 1307
Qy 765 EKAEDSSVOLSTEIPSRSESVSIKFTIPGRKKRADGOKOATVEDSGPEINEDDP 824
Db 1308 DOQAOTQTVINNDONATTEKEAAL-----QOLATA-----VTDANK 1345
Qy 825 NYPAYVPLSEYNAVEREKMEAOGNTELPOLGAVYSEELSKTVHTVSAVIDGTRAVT 884
Db 1346 NITAA---TDDNGVDQAKGAKNSIQSTQPATYKSNAKNDVDQAVTTQNOAIDNTTGAT 1402
Qy 885 SVEERSPSISAVTPELHTAGEAMPVEEYTEKDIIEETPVLTQTLPEBGD-AHDM 943
Db 1403 TEE-----KNAADLVKKAKRAYODILNAQT--TNDVTQIKDOAVADI 1444
Qy 944 VYSEVDTSEAVYATETSEALRTEEVTASGAETTDMYSAV-----SOUTDSPOTTEA 998
Db 1445 OGITADTJTIKVAKDELAKRANOKALLIQTADATTEKEQANOQVDAQIOTGONNIEANA 1504
Qy 999 TPVOEYSEGVLTDEEEROTQAI--LOAVADVKVEESQVPAQTQVQRTSKALEKVEYE 1056
Db 1505 OSIDVNTA-----KDNAIOAIDPIQASTD--VKTNARAEILTEMQ-----NKITEIL 1550
Qy 1057 EDSEVLASKERKDVMPKGVQOEGAHLAOGSTGQATPESLEVPVTAADVHVATCOYI 1116
Db 1551 NNNETTNEKGNDI--GVRAYAYERGL-----NNINAAVTYTGDDVTTAKDJAQV 1596
Qy 1117 KLOQLMEQAV-APESSETLTDESETNGSTPLADSDTADGTQOD-----ETIDSODSKATA 1170
Db 1597 KYOQULHANVKKPAGKKELDQAAADKKTOI--EQTPNASQOELINDAKQOVDTELNAKTN 1654
Qy 1171 VROSOVTEEAATAQKEEPSTLPNNVPAOEHEGEPGRDVLPTQOELTAAAVPVLAKTE 1230
Db 1655 VOQSS--TNEYVNNAYEKGAKI-NAVKTESEYKKD-----ALAKIE 1693
Qy 1231 VQOEGVMDLDEKV-----KEOEYFVHSG----- 1256
Db 1694 DAYNAVNVNADSNASTSSEIAEAKOIAELKOTADONVNOATSKDIDVQIHNDJNIN 1753
Qy 1257 ----PNSOKAA-----DYTDESEVWAGVAGQEKESTEVOSL----- 1288
Db 1754 DYTIPGKKESTATDLXATADOKKNNISADTNAOTDEKQOAIKOVNOVOTALESTINNVO 1813
Qy 1289 -----SLEGBEMETVEKERETKPE-----QVSEGEQETAADEHGTGKVPVLTLD 1336
Db 1814 DNGDVDDALTOGKAIDAIOVATVPRKANOAIIEVKAEDTKESIDQSDQ----- 1862
Qy 1337 MESSERKALGSLGSPSLPDDDKACICIVOVOSLDTTYTQTAEAVER-----VIETV 1389
Db 1863 LPAEETTELAMI--KOITDOAKOGI-----TDAITTTAE-VEKAKOGLAEAFDNI 1909

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Qy 1390 VISETGESEPCVGAHLLPAEKSSATGHWTLQHAEDTVPLG-----PESQAESI 1438
Db 1910 QIDST-----EKOKAIE---ELEFALDOIAGVAVNADATTEKEATNML 1952
Qy 1439 PIIVTPAPESTLHPDLOGEISASQRESESEEDKPDGAPDADKESTAIEKVLKAEPEIL- 1497
Db 1953 EDILSKATEDISDQTTNAEIAFVKNALBQLKQRIINPEVKKNALEAIREVNNKOIEILK 2012
Qy 1498 --ELESKNKIYLVNTQTAVIDOFAKETETAPETHANYSORQ---VPA 1538
Db 2013 MADDASAKEIAFTDQIGRYEDRFADKLDKTOQTNAAVEALQNVITPA 2058

RESULT 12
US-09-919-172-98
; Sequence 98, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OR INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 98
; LENGTH: 3256
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 2700132CD1
US-09-919-172-98

Query Match 4.7%; Score 377; DB 10; Length 3256;
Best Local Similarity 20.2%; Pred. No. 4.9e-09;
Matches 387; Conservative 241; Mismatches 762; Indels 524; Gaps 83;

Qy 14 OPAGSDTPESELYLSGH-----GPAEASGAADPADADPATRLPKNGQL 58
Db 1412 QISGETTHIDKYPGGEDKINAFRETAOKKIDPRASVTSKSNHP-----KTKEAQPL 1464
Qy 59 SSYNGVAGQGDVHVOEENOGQBE-----EYVEDVQOR--ESDVEDREKQVDEM 106
Db 1465 EDLAGKKELEFQTPVCTDKPTTHEKTKIKACRSQPDVPDPTSSKRSLLKRVDEEEL 1524
Qy 107 AANSTAVEDITK-----DGOE-----ETSEIIIOIPASENNVDEMOPAES 147
Db 1525 FALRKRTPSGAKAMHTPKRAVSGEKNITVAFMGTVPQKLDLTNLGSKRRRLQTPREKQA 1584
Qy 148 QANDVGFKKVFEVGFKFTVKKDKNKSDFYOLLTVKKDEGGAES-----VGA 197
Db 1585 LBDLAGFKELFQTRG--HTHEESMTNDKTAKVAKSSQPDLDKNPSSKRLKLTSLGKGV 1642
Qy 198 GDHOEBSVETAVGESAKSEELKOSTEKOETGLKQEOSSTEIPLQAESDQAAEEBAKDEG 257
Db 1643 KEEL-----LAVGKLLQTSGETTHTEPTGDKSKAKMESP-----KOIDSAAISLIG 1692
Qy 258 EKOKEKEPTKSPESPSPVN-----SETTSFKKFTTHGAGARRKTSFPKSKSEDDLETA 313
Db 1693 SKROLTPKGSSEVPDLAGFTELFQTPSHTKESMTNKT---TVASYRASQPDVLVDPPT 1749
Qy 314 KRKEQ---EAEKVDEEEK-----EKTEPAS-----EEOE-----PAEDTQV- 346
Db 1750 SSKPQKRSLRADNDEEELARFKQTPSAGKAMHTPKRAVGEKQINTFLGTPVQKLOP 1809
Qy 347 -----ARLSADYEKVELPLEDOVGDL-----ASSEK-----CAPLATEYFD 384
Db 1810 GNLPGSNRLQTRKEKAQ--ALEELTGFRLEFQTPCTDNPFTDEKTTKILCKSPQSDPAD 1868

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QY 385 -----EKEAHOEYVA--EVHVSTVEKTEEGOGGAEVVEGTESLP 429
Db 1869 TPTNTKORRBSLKADVEEFELAFKLLRPSAGKAMHTPKAANGCEKDLNTPVGT-----P 1924
QY 430 PEKL-----ABPOVPOBAEPABELMKSRMCVSGGDHTO-----LTDLS--- 469
Db 1925 VKLIDLGNLPGSKRRPQTPKEKAKALEDLAGFKELFOTPG--HTEESMTDDKTTEVSCKS 1983
QY 470 --PEKTLKHPGICISVEMLSOERIKVQSP--KFLSSSLKLLSGCKKQKGG 524
Db 1984 POPDPVKT--TSSKORLKLISLGVKVEVLVGLTQTSKTTQTHRE 2031
QY 525 GGDDEEPGEYOHITHESPESA--DEQKGSASSPEEP--EETTLCP-----KGLLAPAD 576
Db 2032 TNGD---GKSIAFKESAAQMDLPANYGGMEMWRTPKKEAQSLEDLAGFKLLPOTPD- 2087
QY 577 GEAEBCGTSDEGKKRGITPWPASFMMVTPKKRVRRP---SESDKEELEKYKSAVTLSS 632
Db 2088 -HTEESTTDDKTKTKACKSP--PPESMDPTPTSTRRRPKTPLGRDIVEELSAKQLQT 2144
QY 633 -TD-----STVSEMDDEVKTIV--GEQKPEEPKRVDTSVSMEAL----- 669
Db 2145 HVDKVPGEDDKGINVFRETAKQKLDPAASVTSKROPTPKAKQPLEDLAGLKELFOTP 2204
QY 670 ICVG-----SSKKRARKASSSDDEGGPRTLGDSHRA-----EASDKKEAGTDAV-- 715
Db 2205 ICTDKRTTHEKTTKICRSPQDPDPVGTPIIFKQSKSLRKADVEESLALKRRTSVGK 2264
QY 716 -----PASTOEDOAQSSSP--EPAGSPSEGGVSTWESFKRLVTPKKSKSLEKAE 768
Db 2265 AMDTPKAGDEKDMKAFMGTPVQKLDLPGNLPGSKRMPQ-----TPKEAQA--LEDLAG 2318
QY 769 DSSVEQLSTEIEPSRESWVSI-----KKFIPRRKKRBDGQKQATVED 813
Db 2319 FKELFOTPGCTDKTTDEKTTKIACKSPQDPDPVDTASTORPRKRNLRKADVEEFLALRK 2378
QY 814 SGFVELNEDDPNPAVVPVLESYNA--VER--EKEAOGN-----TELPOLLGAVY 859
Db 2379 RRPASAKAMDTPRPAVSDEKNITFETVPQKLDLGNLPGSKROQOTPREKALEDLV 2438
QY 860 VSEELSKTLVHYSAVIDGTBAVTVSEERSPSWISASTEPLEHTAGEMAPVEEYTEK 919
Db 2439 GKELFOTPGHTEESMTD--KITEVSOCKSP-----QPSFKTSRSSKORLKIPLV 2487
QY 920 DIIAETTPV---LQTLPEGKAHND-----MYTSEVDFTSSEAVTATETSEALR 965
Db 2488 KYDMKEEPLAVSKLITSGETTQTHTEPTGDSKIAFKESPKQIILDPASVTSGRRLR 2547
QY 966 T-----EVTASGAEE--TTDMVASVSLTDSPTTEATPVQVEESGV 1008
Db 2548 TREKARALEDLVDFKELPSAPGHTEESMTIDKNTKIPCKSPPELIDPATSTRKCPKTR 2607
QY 1009 LQTEEERQTOALQAVADKVEESQVPAQVYQRTGSKALEVEVEEDSEVLASEKER 1068
Db 2608 LRKEVKEE-----LSAVERLYTQSGSTHTHKEPASGDEGIKVKORAKKRPVVEEPS 2662
QY 1069 DVMPKPVQBOA--GAHILA---QGSFQGAQTPES-----LEVPVTADVDH 1109
Db 2663 RRRPRPKKAPQLEDLAGTELSETSGHTQESLTAGKATKIPCSEPPLEVDYTTASTKR 2722
QY 1110 VATQVQIKLQOLEQAVAESSETLTDSETNGSTPLADSDTA----- 1151
Db 2723 HLTRVQKVO-----VKEEPSAVKFTQTSGETTDADKEPAGEDKIGALKESAKQTPA 2775
QY 1152 -----DGTQODETT-----DSQSKATAAARQSOVTEEBA 1182
Db 2776 PAASVTSRRRRPAPRESQAIEDLAGFKDPDPAAGHTEESMTDKTKICKCKSPPELEDTA 2835
QY 1183 TPOKEEPTLPPNVAPQOEHEGEPGRDVLEPTQOELLAAAVPYLAKTEVGESEVMDLG 1242
Db 2836 TSSKRRPRTRAQKVEEKE-----LLAVGKLQOT---SETTHHTDK 2873
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QY 1243 EKVKEQEVFVHSGPNQSAADVTYDSE--VMG-----VACQCKESTE 1284
Db 2874 EPVGECKGTAKFQOPAKRR-----LDAEDVIGSRROPAPRKEKQPLEDLASFOELSGTP 2928
QY 1285 VQSLSEBEME--IDVEKEKRET--KPEVSEEGDEBTAPRHEGIGYKRPVILDMPSSE 1341
Db 2929 GHTEELANAAQSFSTAPAPQTPDSCGPLKTS---RRVLAPRVE--PVGQVSTRD--PVKS 2983
QY 1342 RGAALGSLGSPSLPQDQACGIEVOVQSLDPTVQOTAP-----AVEKIEFTVISETGE 1396
Db 2984 QSKSNTSL--EPLPRKRGG-----KDSVYGTKRLRCMPAPELVEE----- 3024
QY 1397 SPECVGNLLPAREKSATGHTLQHAEDTVPLGPESQAESIPITVTPAPESSTLHPDLQ 1456
Db 3025 -----LPASKK-----QVAPRARKSSEPVIMKRSLTRSAKRIEPAE 3063
QY 1457 EISASORESEEDK--PDGPPADG--KESTALEKYLKAPELLELESKKNKIVLVQTA 1514
Db 3064 ELNSNDKMTNKEBKLODVPENKGISLSRRONKTEAEOQITFEVFLAERIEIN----- 3118
QY 1515 VQOFARTE-----TAPETHAY--DSQTVPACRLDSREPRRCMTKKAKMKRHP 1561
Db 3119 -----RNEKKPKTSPEDMIONPDGAKRPTRDKVTEKRLRSARQNESSOP 3167
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RESULT 13
US-09-764-176-7
; Sequence 7, Application US/09764176
; Patent No. US20020127553A1
; GENERAL INFORMATION:
; APPLICANT: NOTEBORN, Mathieu Hubertus Maria
; APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana Anna Maria
; APPLICANT: ROHN, Jennifer Leigh
; APPLICANT: WEISS, Bettam
; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
; FILE REFERENCE: 472508
; CURRENT APPLICATION NUMBER: US/09/764,176
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Description of Sequence: Amino acid sequence deduced from the
; OTHER INFORMATION: Ictc acid sequence of AAP-
US-09-764-176-7

Query Match          4.6%; Score 368; DB 10; Length 1400;
Best Local Similarity 19.6%; Pred. No. 4.6e-09;
Matches 283; Conservative 226; Mismatches 495; Indels 442; Gaps 65;

QY 95 EDVREKRDVEEAMNASTAVEDI--TKDQGETSEIIEQIPASENNVEENVPQAESQANDV 152
Db 92 DNLKFNINIINEEDADIMRLOPIGRDKGLMYVQLDQ-----DHNVRMYIEQDDQDGS- 145
QY 153 GPKKVKFPGFKTYKKDKNEKSDTYQLLTIVK-----KDEBGAEASVAGADHQEPSVE 206
Db 146 -----SMKCIV--RNNNELAETLALLKAOIDPVLLKNSSQQDNSS-----RESPSE 190
QY 207 TAVGESAKSESELKOSTEOGTILKQOOSTEIPLOAESDQAAE--EPAKDEGEKEOKE 264
Db 191 ----DEETKKEETPROBEKE---SEKMSSEQPMHLENKRSTANVLEETVYKKKEDEKE 244
QY 265 PTK-----SPESPSPVNSSETTSFKKFTFHGAWGAKRTSFKKSKEDDLET--- 311
Db 245 LVKLPVIVLLEKPLPENEEKIIEESDSFKENVK-----PIKVEVKCRADPKDTKSS 298
QY 312 AEKKEQOAEKXD-----EEKEKTEPASEBOBPADTQO-----RLSADYE--- 354
Db 299 MEKPAVOEPERIEFGGNIKSSHEITEKSTETEKLNQOAKIPIPKKREIKLSDDFSPV 358
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[illegible]

QY	1196	VPADEHGECEPRODL-----EPTOO-----ELTAAAVPVLAKTEVSGEGEDWLDGSKV	1245
Db	1331	-----NGOSPEKAIENTLGKFTKSOPTKDNSTASLASNGTSGGDEA-----GAPE	1378
QY	1246	KEEOEV 1251	
Db	1379	EEDDEL 1384	
RESULT 14			
	US-09-963-875-1		
	Sequence 1, Application US/09963875		
	Patent No. US20020164307A1		
	GENERAL INFORMATION:		
	APPLICANT: Massachusetts General Hospital		
	TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treating		
	TITLE OF INVENTION: Mellitus		
	FILE REFERENCE: 17633/1235		
	CURRENT APPLICATION NUMBER: US/09/963,875		
	CURRENT FILING DATE: 2001-09-26		
	PRIOR APPLICATION NUMBER: US60/169082		
	PRIOR FILING DATE: 1999-12-06		
	PRIOR APPLICATION NUMBER: US 60/215109		
	PRIOR FILING DATE: 2000-06-28		
	PRIOR APPLICATION NUMBER: US 60/238880		
	PRIOR FILING DATE: 2000-10-06		
	PRIOR APPLICATION NUMBER: US 09/731261		
	PRIOR FILING DATE: 2000-12-06		
	NUMBER OF SEQ ID NOS: 58		
	SOFTWARE: PatentIn version 3.1		
	SEQ ID NO 1		
	LENGTH: 1618		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US-09-963-875-1		
	Query Match	4.4%, Score 354, DB 9, Length 1618,	
	Best Local Similarity	20.1%, Pred. No. 2,2e+08;	
	Matches 342; Conservative 224; Mismatches 623; Indels 510; Gaps 75;		
QY	133	VKKDGEAGASVSGDHOEVSVERAVGESASKE-----SELKOS--T	223
Db	26	VKALEQNELLSAGLGGRSADTSWRAHADDLEALRALVLDQWRKKAHAEVARDNLA	85
QY	224	EKOEGT-----LKQOSSPREI-----PQAE-----SDQAEEEDANDE-----	256
Db	86	ELBEVAGRCQGLRLARERTTEEVARNRRAYAEKCARAWLSSQCAELERLELALRVANHE	145
QY	257	-----GEEQOEPEPKSPSPSSPVNSETTSSEFKFETHGAG-----WRKTSFKK	303
Db	146	ERVGLINAOACAPRLPAPRPAPAPAVEELARLGEAMGAVNGYQERYVAHHNETSLDQ	205
QY	304	SKEDOLETAEKRKE--QAEKYVDEEEKTEKTPASRGEQPAEDTQARLSADYEVKELPLE	361
Db	206	TRELRARVQAGARERLDLQDLAERGGLLERALLLEGLRGRWQERLRAT--EKFQLAVE	264
QY	362	DOVGLLEASSEKCAPLATEVFEDEKMEAHQVVAEVHST-----VEKTEEOGGG--	413
Db	265	-----ALBEKQGLSQINQVLEGRQOLAHKMLSLSEVATYRTLLAEANSRLQTPGGGSK	320
QY	414	-----BAEGGVVEG--TGESLP--PEKLAEPQEVQDAE--PAEELMKSRMCV	457
Db	321	TLSLSDPEKLELOPFRTPREGRRRLGSLPLVLSPTSL--PSPPLATLETPVPAPFLKNQEFIQ	378
QY	458	SGGHTQTLTDSPEKTLPKHREGVSEVEMLSQERKKNVQSGPLKTLFSSSGLKLSGK	517
Db	379	AKPTPLASTPIRP--TPQAPSPAV-----DAEIRADAPSLSLQDTGGKQAPAP	426
QY	518	KQKGRG-----GDEEP--GEYOHINT--ESPESADBOKESSASPEEPEETKLEKG	569
Db	427	LRAEKRAVAPASVLRGPREFPGGRQDEASTGSPED-----HASTAPPLSPDHS-----	475
QY	570	PLEADQDEAGEEGTT-----SDGEKKREGITP-----WASKKMYTPKKKVRAPSE	615

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Db 476 -LEA-KDSESGSVFYSICRGEGEIOIMGLVERETAIEGKVVSIIQOEIWEEDINRKKEI 533
QY 616 SKEEELKVKATLSTSDSTVSEMODEKVTYGE-----EOKPEPKRVRVTSWML 669
Db 534 QDSQVPLEK---ETLKSIG---EEIOESLKTLENOESHETLEBNOCPRLSEDL--ETL 585
QY 670 ICVGSKKRARRKASSSDDEGPR-----TLGDSHRAEASKDKEA----- 710
Db 586 KSLKENKRAIIGCGSEFSRKRGCROCLKPTGKEDTQTIQSLQKKNQMLKSLGULETF 645
QY 711 ---GTD--AVPASTQEDQD---AQSSSPPEPAGSPSEEGCVS----- 744
Db 646 LPPGTEMOELVSLQENLSTLTALEKENOEPLRSPVGEALRPLTKENOEPLRSLDE 705
QY 745 TWSEFRRLTPPKRSKSKLEEKAEDESVQSLSTE-----TEPSRESWSVSKRTIIPGR 797
Db 706 NKEAFRSLKEKNOEPLKTLTEE-DOSTIVRPLETENHKSRLSEODQETLRILEK--ETQ 762
QY 798 RKRADGKOQATVEDSGFVEINEDDPNVPAYVPLSEYNAVEREKMAQNTLPQLGA 857
Db 763 QRRLSGEDDQMTLRP-----PEKYDLEPLKSLQD----- 793
QY 858 VYVSELSLTVHTVSVAVIDGRAVTSVERNSPWSIASVTEPLEHTGEMAPPEVYT 917
Db 794 -----IARPLENQEPLKSLKEES 813
QY 918 EKDIIAETPVLITQLPEKDAHDMVTSEVDTSEAVTATESEALRTYEVEASGAE 977
Db 814 VEAVSLELEIILSKSAGOE-----NLETLSPEIQAFLWMTPEIINKSGME 861
QY 978 TTDWMSAVQLTSDPDTEATPVQVESEGVLDT-----TEEE 1014
Db 862 SSRKGSRTTGVCGSPRIQPPRG-ESGIIEISGMEPGEFISRGVDEKQSLNEE 920
QY 1015 ERQTOAILDADVAKVEEQ-VPATQTVQRTGSKALEKEVEVEDESV-LASKEDQVMP 1072
Db 921 ENLKEGEYESLRLSEEOELPQSDAVOR-WEDTVEKQOELAQESPPGAGVENDD-- 976
QY 1073 KGPVOAGAENLAQOSETGOATPESLEVEPVNTADV-----HVATCOYIKQOOLMEQA 1125
Db 977 -----EAILNLKRBQDGFTRK--EVEYEGELNATEEYWFPGESHPENPEKRGILVEGA 1029
QY 1126 VAPESSETLIDSETNGS-----TPLADSDTAQTOO---DETIDSODS 1165
Db 1030 SVKGAEGLODPEGSOQYGTPLQAPQGLPEAIEPLVEDDVARPGDQASPEVWLSEPA 1089
QY 1166 KATAV-----ROSQVTEERATPAQKEPESTLPPNNVAQE----- 1200
Db 1090 MGESASAGAPGLQGVGGLDPRGLHTRREYMERPLEEESLEAKRVGLGPRKDLPEAG 1149
QY 1201 ---EHGEERG--RDVLEPTQO---ELTA---AAVPLAKTEVGOEGEVWMLGKEV 1245
Db 1150 LGTEFSELPFKSKNDPEPRREGRESEELAPRGAELAPFAETLGHNGSDAPSWPLGSEE 1209
QY 1246 KEEO-----EYFVHSGPNSQAKADVITYSEVWGVACQOKESTEVOSLSLEEG 1293
Db 1210 AEDVDVPLVSPRYTPILEDAPGLQPAEGSQEAS-WGVQARABAGKVESQOEELGSG 1268
QY 1294 EMETDVEKREKREKPRQVSEEGQELTAPRHE--GTYYGK-----PVLTLMPSSEK 1343
Db 1269 ELPELQOEGEESREB--SEEDLGLTLPDSTPLGFLYLSPTSPRMTPLERSGHPLKEYG 1326
QY 1344 K-----ALGSLG-GSPSLPDODKAG--C-----IEVQVOSLDTIVT-----OTAEA 1381
Db 1327 KEGMDPAVLASEGLEPSEKEKEBEGEBEGCGRSDLSSEEDLGTAPPLPGVPGEYAE 1386
QY 1382 VEKVETVV-----ISETGESPE-----CVGAHLPL 1407
Db 1387 LGQVPLLLDPAWMDRDSDFADAEESEGEDEQDEGREGPAGRWPGSSVGS--LQ 1444
QY 1408 AEKSSATGGHMTLQHAEDVYPLGPESOAESIPIIVTPAPESTLHPDLQ--GEISASORER 1465

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Db 1445 AIISSORGEFLESVSVPWD-----DSLKGAVAGAKTALTEBOSDASPEGSSEES 1499
QY 1466 S-----EEDK-----PDAGPDADGKESTAIIEKYLKAEPLILELSKSNKI---V 1507
Db 1500 DEVSLEREKRYGPLEIPSGMEDADRGAD-----IIGVNGGPNNEGKSHYNGCV 1550
QY 1508 LVNIQTAVDQFARTETAPE 1526
Db 1551 MNGLEQSEESGARNALVSE 1569

RESULT 15
US-09-864-761-36182
; Sequence 36182, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1c9-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36182
; LENGTH: 617
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005529.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

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